#### SEQUENCE LISTING

55

	(1) GE	NERAL INFORMATION:
5	(i)	APPLICANT: Genentech, Inc., Hsei, Vanessa Koumenis, Iphigenia Leong, Steven R. Presta, Leonard G. Shahrokh, Zahra Zapata, Gerardo A.
	(ii)	TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
15	(iii)	NUMBER OF SEQUENCES: 72
20	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Genentech, Inc. (B) STREET: 1 DNA Way (C) CITY: South San Francisco (D) STATE: California (E) COUNTRY: USA (F) ZIP: 94080
25	(v)	COMPUTER READABLE FORM:  (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  (B) COMPUTER: IBM PC compatible  (C) OPERATING SYSTEM: PC-DOS/MS-DOS  (D) SOFTWARE: WinPatin (Genentech)
30	( )	
25		CURRENT APPLICATION DATA:  (A) APPLICATION NUMBER:  (B) FILING DATE: 20-Jan-1999  (C) CLASSIFICATION:
35	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 60/074330 (B) FILING DATE: 22-JAN-1998
40	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 60/094003 (B) FILING DATE: 24-JUL-1998
45	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 60/094013 (B) FILING DATE: 24-JUL-1998
50	(vii)	PRIOR APPLICATION DATA:  (A) APPLICATION NUMBER: 60/075467  (B) FILING DATE: 20-FEB-1998
55	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Love, Richard B. (B) REGISTRATION NUMBER: 34,659 (C) REFERENCE/DOCKET NUMBER: P1085R4-1A

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(ix) TELECOMMUNICATION INFORMATION:
            (A) TELEPHONE: 650/225-5530
            (B) TELEFAX: 650/952-9881
     (2) INFORMATION FOR SEQ ID NO:1:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 base pairs
            (B) TYPE: Nucleic Acid
            (C) STRANDEDNESS: Single
            (D) TOPOLOGY: Linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
      CAGTCCAACT GTTCAGGACG CC 22
15
     (2) INFORMATION FOR SEQ ID NO:2:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 22 base pairs
20
            (B) TYPE: Nucleic Acid
            (C) STRANDEDNESS: Single
            (D) TOPOLOGY: Linear
25
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
      GTGCTGCTCA TGCTGTAGGT GC 22
30
     (2) INFORMATION FOR SEQ ID NO:3:
        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 23 base pairs
            (B) TYPE: Nucleic Acid
35
            (C) STRANDEDNESS: Single
            (D) TOPOLOGY: Linear
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
40
      GAAGTTGATG TCTTGTGAGT GGC 23
     (2) INFORMATION FOR SEQ ID NO:4:
45
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 24 base pairs
             (B) TYPE: Nucleic Acid
             (C) STRANDEDNESS: Single
             (D) TOPOLOGY: Linear
50
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
      GCATCCTAGA GTCACCGAGG AGCC 24
55
     (2) INFORMATION FOR SEQ ID NO:5:
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5	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Single</li><li>(D) TOPOLOGY: Linear</li></ul>
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
10	CACTGGCTCA GGGAAATAAC CC 22
	(2) INFORMATION FOR SEQ ID NO:6:
	(2) INFORMATION FOR SEQ ID NO.0:
15	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 22 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Single</li></ul>
20	(D) TOPOLOGY: Linear
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
" iii	GGAGAGCTGG GAAGGTGTGC AC 22
<b>25</b>	(2) INFORMATION FOR SEQ ID NO:7:
out tour	(i) SEQUENCE CHARACTERISTICS:
<sup>11</sup> 30	<ul><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: Nucleic Acid</li></ul>
- 30	(C) STRANDEDNESS: Single
72 <b>k</b>	(D) TOPOLOGY: Linear
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
Took from	ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35
40	(2) INFORMATION FOR SEQ ID NO:8:
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 35 base pairs</li></ul>
	(B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single
45	(D) TOPOLOGY: Linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
50	ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35
	(2) INFORMATION FOR SEQ ID NO:9:
	(i) SEQUENCE CHARACTERISTICS:
55	<ul><li>(A) LENGTH: 35 base pairs</li><li>(B) TYPE: Nucleic Acid</li></ul>

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(C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
   5
        ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35
       (2) INFORMATION FOR SEQ ID NO:10:
  10
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 37 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
  15
              (D) TOPOLOGY: Linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
  20
        GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGC 37
       (2) INFORMATION FOR SEQ ID NO:11:
          (i) SEQUENCE CHARACTERISTICS:
1 25
              (A) LENGTH: 39 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear
11 30
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
        CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39
1 35
       (2) INFORMATION FOR SEQ ID NO:12:
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 39 base pairs
              (B) TYPE: Nucleic Acid
  40
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
  45
        CGATGGGCCC GGATAGACTG ATGGGGCTGT CGTTTTGGC 39
       (2) INFORMATION FOR SEQ ID NO:13:
  50
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 39 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
             . (D) TOPOLOGY: Linear
  55
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
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	CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39
5	(2) INFORMATION FOR SEQ ID NO:14:
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 39 base pairs</li> <li>(B) TYPE: Nucleic Acid</li> <li>(C) STRANDEDNESS: Single</li> <li>(D) TOPOLOGY: Linear</li> </ul>
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
15	CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39
	(2) INFORMATION FOR SEQ ID NO:15:
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 39 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Single</li></ul>
25	(D) TOPOLOGY: Linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
30	CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39
50	(2) INFORMATION FOR SEQ ID NO:16:
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 369 base pairs</li> <li>(B) TYPE: Nucleic Acid</li> <li>(C) STRANDEDNESS: Double</li> <li>(D) TOPOLOGY: Linear</li> </ul>
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
	GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50
45	CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100
	CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150
	TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200
50	TGGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250
	CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300
55	GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350

CATCTTCCCA CCATTCGAA 369

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	5	(1	( <i>I</i>	A) LI 3) Ti	NCE ( ENGTH YPE: OPOL(	H: 12 Amir	23 ar no Ac	nino cid	ics: acid	is						
	10	(x)	.) SI	EQUE	NCE I	DESCI	RIPT	ON:	SEQ	ID N	10:17	7 :				
	10	Asp 1	Ile	Val	Met	Thr 5	Gln	Ser	Gln	Lys	Phe 10	Met	Ser	Thr	Ser	Val
	15	Gly	Asp	Arg	Val	Ser 20	Val	Thr	Cys	Lys	Ala 25	Ser	Gln	Asn	Val	Gly 30
		Thr	Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Gln	Ser	Pro	Lys 45
17	20	Ala	Leu	Ile	Tyr	Ser 50	Ser	Ser	Tyr	Arg	Туr 55	Ser	Gly	Val	Pro	Asr 60
Actual Bases Base	25	Arg	Phe	Thr	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Leu	Thr	Ile 75
Water than there		Ser	His	Val	Gln	Ser 80	Glu	Asp	Leu	Ala	Asp 85	Туr	Phe	Cys	Gln	Glr 90
14	30	Tyr	Asn	Ile	Tyr	Pro 95	Leu	Thr	Phe	Gly	Pro 100	Gly	Thr	Lys	Leu	Glu 105
11 ±		Leu	Lys	Arg	Ala	Asp 110	Ala	Ala	Pro	Pro	Thr 115	Val	Ser	Ile	Phe	Pro 120
The Party Sent	35	Pro	Phe	Glu 123												
:: A		(2) ]	NFO	RMAT:	ION I	FOR S	SEQ :	ID N	0:18	:						
•	40	<b>i)</b>	(1	A) L: B) T' C) S'	YPE: TRANI	H: 41 Nucl DEDNI	17 ba leic ESS:	ase p Acid Doul	pairs d	5						
	45	(xi			OPOLO				SEQ	ID 1	NO:1	8:				
	50	TTCT	TATT	GCT I	ACAA	ACGC(	GT A	CGCT	GAGG:	r GC	AGCT(	GGTG	GAG'	rctgo	GGG :	50
	50	GAGO	GCTT/	AGT (	GCCG	CTG	GA G	GGTC	CCTG	AA A	CTCT	CCTG	TGC	AGCC'	rct :	100
		GGAT	PTCA:	TAT '	TCAG:	PAGT'	TA TO	GGCA!	rgrc	r TGC	GGTT(	CGCC	AGA	CTCC	AGG	150
	55	CAAC	GAGC	CTG (	GAGT	rggto	CG C	AACC	ATTA	A TAA	'AATA	rggt	GAT	AGCA	CT :	200

(2) INFORMATION FOR SEQ ID NO:17:

	ATTA	TCC	AGA (	CAGT	GTGA	AG G	GCCG	ATTC	A CC	ATCT(	CCCG	AGA	CAATO	GCC :	250
	AAGA	ACA	cc r	rgta	CCTG	CA A	ATGA	GCAG!	r ctc	GAAG!	rctg	AGG	ACACA	AGC	300
5	CATG	TTT	rac :	rgtgo	CAAG	AG C	CCTC	ATTA	G TTC	CGGC	TACT	TGG	rttgo	3TT	350
	ACTG	GGGG	CCA A	AGGG	ACTC	rg g	rcac'	rgrc:	r cto	GCAG	CCAA	AAC	AACAG	SCC ·	400
10	CCAT	CTG	rct A	ATCC	GGG 4	417									
10	(2) I	NFO	RMAT:	ION 1	FOR :	SEQ :	ID N	0:19	:						
15	(i	( I	A) LI B) T	ENGTI YPE :		30 ai	cid	ICS: acid	is						
	(xi	) SI	EQUE	NCE I	DESCI	RIPT:	ION:	SEQ	ID 1	10:19	9:				
20	Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Pro	Pro	Gly 15
1 25	Gly	Ser	Leu	Lys	Leu 20	Ser	Суѕ	Ala	Ala	Ser 25	Gly	Phe	Ile	Phe	Ser 30
1000 und your	Ser	Tyr	Gly	Met	Ser 35	Trp	Val	Arg	Gln	Thr 40	Pro	Gly	Lys	Ser	Leu 45
<sup>1</sup> 30	Glu	Leu	Val	Ala	Thr 50	Ile	Asn	Asn	Asn	Gly 55	Asp	Ser	Thr	Tyr	Tyr 60
***		Asp	Ser	Val	Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ala 75
35	Lys	Asn	Thr	Leu	Туr 80	Leu	Gln	Met	Ser	Ser 85	Leu	Lys	Ser	Glu	Asp 90
40					95			Arg		100					105
			-	_	110			Gly		115	Val	Thr	Val	Ser	Ala 120
45		_			125			Val	_	Pro 130					
	(2) I	NFO	TAMS	ION I	FOR S	SEQ :	ID NO	0:20:	:						
50	(i	() ()	A) LE 3) TY C) ST	ENGTI PE: PRANI	1: 3: Nuc:	l bas leic ESS:	RIST: se pa Acio Sino sar	airs 1							
55	(xi	) SI	EQUE	NCE I	DESC	RIPT	ON:	SEQ	ID N	IO:20	):				

```
ACAAACGCGT ACGCTGATAT CGTCATGACA G 31
      (2) INFORMATION FOR SEQ ID NO:21:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 31 base pairs
             (B) TYPE: Nucleic Acid
             (C) STRANDEDNESS: Single
 10
             (D) TOPOLOGY: Linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
 15
       GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31
      (2) INFORMATION FOR SEQ ID NO:22:
         (i) SEQUENCE CHARACTERISTICS:
. 20
             (A) LENGTH: 21 base pairs
             (B) TYPE: DNA
             (C) STRANDEDNESS: Single
             (D) TOPOLOGY: Linear
1 25
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
       CCACTAGTAC GCAAGTTCAC G 21
 30
      (2) INFORMATION FOR SEQ ID NO:23:
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 33 base pairs
             (B) TYPE: Nucleic Acid
35
             (C) STRANDEDNESS: Single
             (D) TOPOLOGY: Linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
 40
       GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33
      (2) INFORMATION FOR SEQ ID NO:24:
 45
         (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 714 base pairs
             (B) TYPE: Nucleic Acid
             (C) STRANDEDNESS: Double
             (D) TOPOLOGY: Linear
 50
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
       ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50
 55
       TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100
```

	TGTCCACATC	AGTAGGAGA	AC AGGGTC	:AGCG '	TCACCTG	CAA	GGCC	AGTC	AG .	150
5	AATGTGGGTA	CTAATGTAC	SC CTGGT	ATCAA (	CAGAAAC	CAG	GGCA	ATCT	CC :	200
3	TAAAGCACTG	ATTTACTCO	T CATCC	ACCG (	GTACAGT	GGA	GTCC	CTGA	TC :	250
	GCTTCACAGG	CAGTGGAT	T GGGACA	AGATT '	TCACTCT	CAC	CATC	AGCC	AT :	300
10	GTGCAGTCTG	AAGACTTG	GC AGACTA	ATTTC '	TGTCAGC	TAA	AATA	CATC	TA:	350
	TCCTCTCACG	TTCGGTCCT	rg ggacca	AAGCT (	GGAGCTT	CGA	AGAG	CTGT	GG ·	400
16	CTGCACCATC	TGTCTTCAT	rc TTCCC	CCAT	CTGATGA	GCA	GTTG	LAAA	CT ·	450
15	GGAACTGCTT	CTGTTGTGT	rg cctgc	GAAT .	AACTTCT	ATC	CCAG	AGAG	GC	500
	CAAAGTACAG	TGGAAGGT	G ATAACO	SCCCT (	CCAATCG	GGT	AACT	CCCA	.GG	550
20	AGAGTGTCAC	AGAGCAGG	AC AGCAAC	GACA (	GCACCTA	CAG	CCTC	AGCA	.GC	600
	ACCCTGACGC	TGAGCAAA	GC AGACTA	ACGAG	AAACACA	AAG	тста	.CGCC	TG	650
25	CGAAGTCACC	CATCAGGG	CC TGAGC	rcgcc	CGTCACA	AAG	AGCT	TCA.	CA	700
23	GGGGAGAGTG	TTAA 714								
	(2) INFORMA	TION FOR	SEQ ID NO	):25:						
30	(A) (B)	ENCE CHARA LENGTH: 2: TYPE: Amin TOPOLOGY:	37 amino no Acid							
35	(xi) SEQU	ENCE DESCI	RIPTION:	SEQ I	D NO:25	:				
	Met Lys Ly 1	s Asn Ile 5	Ala Phe	Leu L	eu Ala 10	Ser	Met	Phe	Val	Phe 15
40	Ser Ile Al	a Thr Asn 20	Ala Tyr	Ala A	sp Ile 25	Val	Met	Thr	Gln	Ser 30
45	Gln Lys Ph	ne Met Ser 35	Thr Ser	Val G	ly Asp 40	Arg	Val	Ser	Val	Thr 45
43	Cys Lys Al	a Ser Gln 50	Asn Val	Gly T	hr Asn 55	Val	Ala	Trp	Tyr	Glr 60
50	Gln Lys Pr	o Gly Gln 65	Ser Pro	Lys A	la Leu 70	Ile	Tyr	Ser	Ser	Sez 75
	Tyr Arg Ty	r Ser Gly 80	Val Pro	Asp A	rg Phe 85	Thr	Gly	Ser	Gly	Ser 90
55	Gly Thr As	p Phe Thr 95	Leu Thr	Ile S	er His 100	Val	Gln	Ser	Glu	Asp 105

	Leu	Ala	Asp	Tyr	Phe 110	Суѕ	Gln	Gln	Tyr	Asn 115	Ile	Tyr	Pro	Leu	Th:
5	Phe	Gly	Pro	Gly	Thr 125	Lys	Leu	Glu	Leu	Arg 130	Arg	Ala	Val	Ala	Ala 135
10	Pro	Ser	Val	Phe	Ile 140	Phe	Pro	Pro	Ser	Asp 145	Glu	Gln	Leu	Lys	Ser 150
10	Gly	Thr	Ala	Ser	Val 155	Val	Суѕ	Leu	Leu	Asn 160	Asn	Phe	Tyr	Pro	Arg 165
15	Glu	Ala	Lys	Val	Gln 170	Trp	Lys	Val	Asp	Asn 175	Ala	Leu	Gln	Ser	Gl <sub>3</sub> 180
	Asn	Ser	Gln	Glu	Ser 185	Val	Thr	Glu	Gln	Asp 190	Ser	Lys	Asp	Ser	Th: 199
20	Tyr	Ser	Leu	Ser	Ser 200	Thr	Leu	Thr	Leu	Ser 205	Lys	Ala	Asp	Tyr	Glu 210
25	Lys	His	Lys	Val	Туг 215	Ala	Суѕ	Glu	Val	Thr 220	His	Gln	Gly	Leu	Ser 225
23	Ser	Pro	Val	Thr	Lys 230	Ser	Phe	Asn	Arg	Gly 235	Glu	Cys 237			
30		i) Si (i	EQUEI A) Li B) T	NCE ( ENGTI YPE:	CHARA H: 7! Nuc:	ACTE 56 ba	RIST: ase p Acid	pairs d					•		
35	•			TRANI OPOLO				ble							
	(x	i) S	EQUE	NCE I	DESCI	RIPT:	ION:	SEQ	ID I	NO : 2	6:				
40	ATG.	AAAA	AGA Z	TATA	CGCA'	rt to	CTTC	TTGC#	A TC	ratg:	rtcg	TTT	rttc	TAT	50
								CAGCT							
45				•				ACTCT							
								gggti aata <i>i</i>							
50								CATC							
								rgaac							
	TTA	CTGT	GCA 2	AGAG	CCCT	CA T'	TAGT'	rcgg	TAC	CTTG	GTTT	GGT	racto	GGG	400
55	GCC	AAGG	<b>3</b> ልሮ '	<u></u> ኮርጥር (	<b>ታ</b> ሞር <b>አ</b> ሳ	ים יוים	<u> </u>	TGCAC	י ררי	rcca	CCAA	GGG	CCCA	TCG	450

	GTCTTCC	ccc '	TGGC	ACCC1	rc c	rcca.	AGAG	C AC	CTCT	GGGG	GCA	CAGC	GGC	500
£	CCTGGG	CTGC	CTGG	TCAA	GG A	CTAC	rtcc	C CG/	AACC	GTG	ACG	GTGT	CGT	550
5	GGAACTO	CAGG	CGCC	CTGA	CC A	GCGGG	CGTG	C AC	ACCT	rccc	GGC	rgtc	CTA	600
	CAGTCCT	rcag (	GACT	CTAC	rc co	CTCAC	GCAG	C GTY	GGTG	ACCG	TGC	CCTC	CAG	650
10	CAGCTTC	GGC .	ACCC	AGAC	A TO	CATC	rgca	A CG	rgaa'	CAC	AAG	CCA	GCA	700
	ACACCA	GGT (	GGAC	AAGA	AA G	rtga(	GCCC	A AA	rctt	STGA	CAA	AACT	CAC	750
15	ACATGA	756												
.,	(2) INFO	RMAT	ION 1	FOR S	SEQ :	ID NO	0:27	:						
20	(	SEQUE (A) L (B) T (D) T	ENGT YPE:	H: 29 Amin	51 ar	mino cid		ds						
	(xi) S	SEQUE:	NCE 1	DESCI	RIPT	ON:	SEQ	ID I	10 : 2 °	7:				
25	Met Lys 1	. Lys	Asn	Ile 5	Ala	Phe	Leu	Leu	Ala 10	Ser	Met	Phe	Val	Phe 15
	Ser Ile	e Ala	Thr	Asn 20	Ala	Tyr	Ala	Glu	Val 25	Gln	Leu	Val	Glu	Ser 30
30	Gly Gl	y Gly	Leu	Val 35	Pro	Pro	Gly	Gly	Ser 40	Leu	Lys	Leu	Ser	Cys 45
35	Ala Ala	a Ser	Gly	Phe 50	Ile	Phe	Ser	Ser	Tyr 55	Gly	Met	Ser	Trp	Val 60
	Arg Glr	1 Thr	Pro	Gly 65	Lys	Ser	Leu	Glu	Leu 70	Val	Ala	Thr	Ile	Asn 75
40	Asn Asr	ı Gly	Asp	Ser 80	Thr	Tyr	Tyr	Pro	Asp 85	Ser	Val	Lys	Gly	Arg 90
45	Phe Thr	: Ile	Ser	Arg 95	Asp	Asn	Ala	Lys	Asn 100	Thr	Leu	Tyr	Leu	Gln 105
	Met Ser	Ser	Leu	Lys 110	Ser	Glu	Asp	Thr	Ala 115	Met	Phe	Tyr	Суѕ	Ala 120
50	Arg Ala	ı Leu	Ile	Ser 125	Ser	Ala	Thr	Trp	Phe 130	Gly	Tyr	Trp	Gly	Gln 135
	Gly Thr	Leu	Val	Thr 140	Val	Ser	Ala	Ala	Ser 145	Thr	Lys	Gly	Pro	Ser 150
55	Val Phe	Pro	Leu	Ala 155	Pro	Ser	Ser	Lys	Ser 160	Thr	Ser	Gly	Gly	Thr 165

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	Ala Ala L	eu Gly	Cys Leu 170	Val	Lys	Asp	Tyr 175	Phe	Pro	Glu	Pro	Val 180
5	Thr Val S	er Trp	Asn Ser 185	Gly	Ala	Leu	Thr 190	Ser	Gly	Val	His	Thr 195
10	Phe Pro A	la Val	Leu Gln 200	Ser	Ser	Gly	Leu 205	Tyr	Ser	Leu	Ser	Ser 210
	Val Val T	hr Val	Pro Ser 215	Ser	Ser	Leu	Gly 220	Thr	Gln	Thr	Tyr	Ile 225
15	Cys Asn V	al Asn	His Lys 230	Pro	Ser	Asn	Thr 235	Lys	Val	Asp	Lys	Lys 240
	Val Glu P	ro Lys	Ser Cys 245	Asp	Lys	Thr	His 250					
20	(2) INFORM	NOITAL	FOR SEQ	ID N	0:28	:						
25	(A) (B) (C)	LENGTH TYPE: STRANI	CHARACTE H: 37 ba Nucleic DEDNESS: DGY: Lir	se pa Acia Sina	airs d							
	(xi) SEQ	QUENCE I	DESCRIPT	:NOI	SEQ	ID 1	NO:28	3:				
30	CCAATGCAT	ra CGCT	GACATC C	TGAT	GACC	C AG	ACCC	37				
	(2) INFORM	ATION I	FOR SEQ	ID N	0:29	:						
35	(A) (B) (C)	LENGTE TYPE: STRANI	CHARACTE H: 37 ba Nucleic DEDNESS: DGY: Lir	se p Aci Sin	airs d							
40	(xi) SEQ	QUENCE I	DESCRIPT	CION:	SEQ	ID I	NO:2	9 :				
45	CCAATGCAT						ACTC	c 37				
	(2) INFORM					:						
50	(A) (B) (C)	LENGTI TYPE: STRANI	CHARACTE H: 37 ba Nucleic DEDNESS: DGY: Lir	se p Aci Sin	airs d							
<i>e e</i>	(xi) SEQ	QUENCE I	DESCRIPT	: NOI	SEQ	ID 1	NO:3	0 :				

	CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37
	(2) INFORMATION FOR SEQ ID NO:31:
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 35 base pairs</li> <li>(B) TYPE: Nucleic Acid</li> <li>(C) STRANDEDNESS: Single</li> <li>(D) TOPOLOGY: Linear</li> </ul>
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
15	AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35
13	(2) INFORMATION FOR SEQ ID NO:32:
20	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 32 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Single</li><li>(D) TOPOLOGY: Linear</li></ul>
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
	CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32
30	(2) INFORMATION FOR SEQ ID NO:33:  (i) SEQUENCE CHARACTERISTICS:
35	(A) LENGTH: 32 base pairs (B) TYPE: Nucleic Acid (C) STRANDEDNESS: Single (D) TOPOLOGY: Linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
40	CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32
	(2) INFORMATION FOR SEQ ID NO:34:
45	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 391 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Double</li><li>(D) TOPOLOGY: Linear</li></ul>
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
	GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGGAGA 50
55	TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100

	GAA	ACAC	TA T	OATT	CATTO	G TA	CCTC	CAGA	AGC	CAGO	CCA	GTCT	CCAA	AG :	150
	CTC	CTGA	rct a	CAAA	\GTT1	rc ca	ACCG	TTTA	TCT	GGGG	STCC	CAGA	CAGO	STT :	200
5	CAG	rggc	AGT (	GATO	CAGGG	GA CA	GATI	TCAC	ACT	CAGO	SATC	AGC	GAGI	rgg :	250
	AGG	CTGA	GGA 1	rctgo	GACT	T T	\TTTC	TGCT	r crc	CAAAC	TAC	ACA	GTTC	CG :	300
••	CTC	ACGT	rcg (	GTGCI	rggga	AC CA	AAGCI	rggac	CTC	)AAA	GGG	CTG	TGCI	GC :	350
10	ACC	AACTO	GTA 1	rccan	CTTC	CC C	ACCAT	CCAC	G TGA	AGCA.	ATTG	A 39	1		
	(2)	INFO	RMATI	ON F	FOR S	SEQ :	D NO	35:	:						
15	(:	() (1	EQUENA) LI B) TY D) T(	engti Pe :	H: 13 Amir	31 ar no Ac	nino		is						
20	(x:	i) S	EQUE	NCE I	DESC	RIPT	ON:	SEQ	ID N	10:35	5:				
	Asp 1	Ile	Val	Met	Thr 5	Gln	Thr	Pro	Leu	Ser 10	Leu	Pro	Val	Ser	Leu 15
25	Gly	Asp	Gln	Ala	Ser 20	Ile	Ser	Cys	Arg	Ser 25	Ser	Glņ	Ser	Leu	Val 30
30	His	Gly	Ile	Gly	Asn 35	Thr	Tyr	Leu	His	Trp 40	Tyr	Leu	Gln	Lys	Pro 45
	Gİy	Gln	Ser	Pro	Lys 50	Leu	Leu	Ile	Tyr	Lуs 55	Val	Ser	Asn	Arg	Phe 60
35	Ser	.Gly	Val	Pro	Asp 65	Arg	Phe	Ser	Gly	Ser 70	Gly	Ser	Gly	Thr	Asp 75
	Phe	Thr	Leu	Arg	Ile 80	Ser	Arg	Val	Glu	Ala 85	Glu	Asp	Leu	Gly	Leu 90
40	Tyr	Phe	Cys	Ser	Gln 95	Ser	Thr	His	Val	Pro 100	Leu	Thr	Phe	Gly	Ala 105
45	Gly	Thr	Lys	Leu	Glu 110		Lys	Arg		Asp 115	Ala	Ala	Pro	Thr	Val 120
	Ser	Ile	Phe	Pro	Pro 125	Ser	Ser	Glu	Gln		Lys 131				
50	(2)	INFO	RMAT:	ION 1	FOR :	SEQ	ID N	0:36	:						
	(	(. (:	EQUE A) L B) T C) S	ENGTI YPE :	H: 40	05 b leic	ase p Acid	pair: d	s						

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

5	GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50
J	AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTCAGT AGCCACTACA 100
	TGCACTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGCTAC 150
10	ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200
	GGCCACATTG ACTGTAGACA CATCTTCCAG CACAGCCAAC GTGCATCTCA 250
15	GCAGCCTGAC ATCTGATGAC TCTGCAGTCT ATTTCTGTGC AAGAGGGGAC 300
15	TATAGATACA ACGGCGACTG GTTTTTCGAT GTCTGGGGCG CAGGGACCAC 350
	GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400
20	CCATC 405
Thurst Mary	(2) INFORMATION FOR SEQ ID NO:37:
25	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 135 amino acids</li><li>(B) TYPE: Amino Acid</li><li>(D) TOPOLOGY: Linear</li></ul>
<sup>1</sup> 30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
.h	Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly 1 5 10
35	Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser 20 25 30

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Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn Gly Glu Thr Thr Tyr 40

Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser

Ser His Tyr Met His Trp Val Lys Gln Ser His Gly Lys Ser Leu

Ser Ser Thr Ala Asn Val His Leu Ser Ser Leu Thr Ser Asp Asp

Ser Ala Val Tyr Phe Cys Ala Arg Gly Asp Tyr Arg Tyr Asn Gly

Asp Trp Phe Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val

Ser Ser Ala Lys Thr Asp Ser Pro Ile Gly Leu Ser Gly Pro Ile 130

```
(2) INFORMATION FOR SEQ ID NO:38:
          (i) SEQUENCE CHARACTERISTICS:
  5
              (A) LENGTH: 22 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear
  10
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
       CTTGGTGGAG GCGGAGGAGA CG 22
 15
      (2) INFORMATION FOR SEQ ID NO:39:
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 38 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
 20
              (D) TOPOLOGY: Linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
 <sup>1</sup>25
       GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38
       (2) INFORMATION FOR SEQ ID NO:40:
<sup>1)</sup> 30
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 31 base pairs
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Single
              (D) TOPOLOGY: Linear
35
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
       GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31
  40
       (2) INFORMATION FOR SEQ ID NO:41:
          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 729 base pairs
  45
              (B) TYPE: Nucleic Acid
              (C) STRANDEDNESS: Double
              (D) TOPOLOGY: Linear
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
  50
        ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50
        TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100
  55
        TGCCTGTCAG TCTTGGAGAT CAGGCCTCCA TCTCTTGCAG ATCTAGTCAG 150
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	AGCC	rtgt	'AC A	ACGG'I	OT"TA	G AA	AACAC	CTAT	TTA	ACAT"	rggt	ACC'	rgcac	BAA	200
5	GCCAC	GCC	AG 1	CTCC	CAAAC	C TO	CTG	ATCT?	CA	AAGT"	rtcc	AAC	GATT	TT	250
,	CTGGC	GTC	CC A	AGACA	AGGTT	OA OT	GTGG	CAGTO	GAT	rcago	GGAC	AGA	TTC	ACA	300
	CTCAC	GAT	'CA (	GCAGA	AGTGC	GA GO	GCTG/	AGGAT	CTC	GGA	CTTT	ATT	rctgo	CTC	350
10	TCAA	AGTA	.CA (	CATGI	TCC	SC TO	CACG	TCGC	TGO	TGG	GACC	AAG	TGG	AGC	400
	TGAA	ACGG	GC 1	rgttc	CTGC	CA CO	CAACT	CTAT	TC	ATCT	rccc	ACCA	ATCCA	AGT	450
15	GAGC	TTA	'GA A	ATCI	(GGA	C TO	CCT	CTGTT	GTO	STGC	CTGC	TGA	)AATA	CTT	500
	CTATO	CCA	GA C	SAGGO	CAAA	AG TA	ACAGI	KADD1	GG1	rggan	DAAT	GCC	CTCC	ΛAΤ	550
	CGGG	raac	TC (	CAGO	SAGAC	er Gi	rcaca	AGAGO	AGC	GACAC	GCAA	GGA	CAGC	ACC	600
20	TACAC	GCCI	CA (	GCAGO	CACCO	CT GA	ACGCT	rgago	AA.	AGCAC	SACT	ACG	AGAA	ACA	650
	CAAA	GTCT	'AC C	CCTC	GCGAA	AG TO	CACC	CATCA	GG(	CCTC	GAGC	TCG	CCCG	CA	700
25	CAAA	GAGC	TT C	CAACA	AGGGG	A GA	AGTGT	AATT	729	•					
	(2) II	NFOR	TAME:	ON E	FOR S	SEQ I	ID NO	0:42:							
	(i)		-				RIST: mino		is						
30			•	PE: OPOLO											
	(xi)	) SE	QUEI	NCE I	DESCE	RIPT	ION:	SEQ	ID 1	10:42	2:				
35	Met 1	Lys	Lys	Asn	Ile 5	Ala	Phe	Leu	Leu	Ala 10	Ser	Met	Phe	Val	Phe 15
40	Ser :	Ile	Ala	Thr	Asn 20	Ala	Tyr	Ala	Asp	Ile 25	Val	Met	Thr	Gln	Thr 30
40	Pro 1	Leu	Ser	Leu	Pro 35	Val	Ser	Leu	Gly	Asp 40	Gln	Ala	Ser	Ile	Ser 45
45	Cys 1	Arg	Ser	Ser	Gln 50	Ser	Leu	Val	His	Gly 55	Ile	Gly	Asn	Thr	Tyr 60
	Leu I	His	Trp	Tyr	Leu 65	Gln	Lys	Pro	Gly	Gln 70	Ser	Pro	Lys	Leu	Leu 75
50	Ile ?	Fyr	Lys	Val	Ser 80	Asn	Arg	Phe	Ser	Gly 85	Val	Pro	Asp	Arg	Phe 90
55	Ser (	Gly	Ser	Gly	Ser 95	Gly	Thr	Asp	Phe	Thr 100	Leu	Arg	Ile	Ser	Arg 105
	Val (	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr

					110					115					120
		Val	Pro	Leu	Thr 125	Phe	Gly	Ala	Gly	Thr 130	Lys	Leu	Glu	Leu	Lys 135
5		Ala	Val	Ala	Ala 140	Pro	Thr	Val	Phe	Ile 145	Phe	Pro	Pro	Ser	Ser 150
10		Gln	Leu	Lys	Ser 155	Gly	Thr	Ala	Ser	Val 160	Val	Cys	Leu	Leu	Asn 165
	Asn	Phe	Туг	Pro	Arg 170	Glu	Ala	Lys	Val	Gln 175	Trp	Lys	Val	Asp	Asn 180
15	Ala	Leu ·	Gln	Ser	Gly 185	Asn	Ser	Gln	Glu	Ser 190	Val	Thr	Glu	Gln	Asp 195
20		Lys	Asp	Ser	Thr 200	Tyr	Ser	Leu	Ser	Ser 205	Thr	Leu	Thr	Leu	Ser 210
20		Ala	Asp	Tyr	Glu 215	Lys	His	Lys	Val	Tyr 220	Ala	Cys	Glu	Val	Thr 225
2.5		Gln	Gly	Leu	Ser 230	Ser	Pro	Val	Thr	Lys 235	Ser	Phe	Asn	Arg	Gly 240
ma, man ma	Glu	Cys 242													
3(	(2)	INFO	RMAT	ION	FOR :	SEQ	ID N	0:43	:						
3:	·	· (	A) L B) T C) S	ENGT YPE: TRAN	H: 7	62 b leic ESS:	ase p Acid Doub	pair: d	5						
į	(×	i) S	EQUE	NCE :	DESC	RIPT	ION:	SEQ	ID :	NO : 4	3:				
40		AAAA	AGA .	ТАТА	CGCA'	тт т	CTTC'	TTGC	A TC	TATG	TTCG	TTT	TTTC	тат	50
	TGC	TACA	AAC	GCGT	ACGC'	TG A	GATT	CAGC'	r GC	AGCA	GTCT	GGA	CCTG	AGC	100
4:	5 TGA	TGAA	GCC	TGGG	GCTT	CA G	TGAA	GATA'	r cc	TGCA	AGGC	TTC	TGGT	TAT	150
	TCA	TTCA	GTA	GCCA	CTAC.	AT G	CACT	GGGT	G AA	GCAG	AGCC	ATG	GAAA	GAG	200
5		TGAG	TGG	ATTG	GCTA	СА Т	TGAT	CCTT	C CA	atgg	TGAA	ACT	ACTT.	ACA	250
,ر	-	AGAA	TTA	CAAG	GGCA	AG G	CCAC	ATTG.	A CT	GTAG	ACAC	ATC	TTCC	AGC	300
	ACA	AGCCA	ACG	TGCA	TCTC	AG C	AGCC	TGAC.	A TC	TGAT	GACT	CTG	CAGT	СТА	350
5	5 TTI	CTGT	GCA	AGAG	GGGA	ст а	TAGA	TACA	A CG	GCGA	CTGG	TTT	TTCG	ATG	400

	TCTGGGGCGC	AGGGACCAC	G GTCACO	CGTCT	CCTCCGC	CTC	CACC	AAGG	GC	450
	CCATCGGTCT	TCCCCTG	SC ACCCTO	CCTCC	AAGAGCA	ACCT	CTGG	GGGC	AC	500
5	AGCGGCCCTG	GCTGCCTC	G TCAAGO	GACTA	СТТСССС	GAA	CCGG	TGAC	:GG	550
	TGTCGTGGAA	CTCAGGCGG	CC CTGAC	CAGCG	GCGTGC	ACAC	CTTC	CCGG	CT	600
10	GTCCTACAGT	CCTCAGGA	ст стасто	CCTC	AGCAGCG	STGG	TGAC	CGTG	CC	650
10	CTCCAGCAGC	TTGGGCAC	CC AGACC	FACAT	CTGCAAC	CGTG	AATO	ACAA	GC	700
	CCAGCAACAC	CAAGGTGG	AC AAGAA	AGTTG	AGCCCAA	ATC	TTGT	GACA	AA.	750
15	ACTCACACAT	GA 762								
	(2) INFORMA	ATION FOR	SEQ ID NO	0:44:						
20	(A) (B)	JENCE CHARA LENGTH: 29 TYPE: Amin TOPOLOGY:	33 amino no Acid		5					
25	(xi) SEQU	JENCE DESCI	RIPTION:	SEQ I	ID NO:44	<b>1</b> :				
23	Met Lys Ly 1	s Asn Ile 5	Ala Phe	Leu I	Ceu Ala 10	Ser	Met	Phe	Val	Phe 15
30	Ser Ile Al	la Thr Asn 20	Ala Tyr	Ala (	Glu Île 25	Gln	Leu	Gln	Gln	Ser 30
,	Gly Pro Gl	lu Leu Met 35	Lys Pro	Gly A	Ala Ser 40	Val	Lys	Ile	Ser	Cys 45
35	Lys Ala Se	er Gly Tyr 50	Ser Phe	Ser S	Ser His 55	Tyr	Met	His	Trp	Val
40	Lys Gln Se	er His Gly 65	Lys Ser	Leu (	Glu Trp 70	Ile	Gly	Tyr	Ile	Asp 75
70	Pro Ser As	sn Gly Glu 80	Thr Thr	Tyr A	Asn Gln 85	Lys	Phe	Lys	Gly	Lys 90
45	Ala Thr Le	eu Thr Val 95	Asp Thr	Ser S	Ser Ser 100	Thr	Ala	Asn	Val	His 105
	Leu Ser Se	er Leu Thr 110	Ser Asp	Asp S	Ser Ala 115	Val	Tyr	Phe	Cys	Ala 120
50	Arg Gly As	sp Tyr Arg 125	Tyr Asn	Gly A	Asp Trp 130	Phe	Phe	Asp	Val	Trp 135
55	Gly Ala Gl	ly Thr Thr 140	Val Thr	Val S	Ser Ser 145	Ala	Ser	Thr	Lys	Gly 150
JJ	Pro Ser Va	al Phe Pro	Leu Ala	Pro S	Ser Ser	Lys	Ser	Thr	Ser	Gly

					155					160					165
_	Gly	Thr	Ala	Ala	Leu 170	Gly	Cys	Leu	Val	Lys 175	Asp	Tyr	Phe	Pro	Glu 180
5	Pro	Val	Thr	Val	Ser 185	Trp	Asn	Ser	Gly	Ala 190	Leu	Thr	Ser	Gly	Val 195
10	His	Thr	Phe	Pro	Ala 200	Val	Leu	Gln	Ser	Ser 205	Gly	Leu	Tyr	Ser	Leu 210
	Ser	Ser	Val	Val	Thr 215	Val	Pro	Ser	Ser	Ser 220	Leu	Gly	Thr	Gln	Thr 225
15	Tyr	Ile	Cys	Asn	Val 230	Asn	His	Lys	Pro	Ser 235	Asn	Thr	Lys	Val	Asp 240
20	Lys	Lys	Val	Glu	Pro 245	Lys	Ser	Cys	Asp	Lys 250	Thr	His	Thr 253		
20	(2)	INFO	RMAT	ION I	FOR S	SEQ :	ID N	0:45	:						
25	(:	(1	A) Li B) T'		H: 1: Ami	14 ar			ds						
	(x:	i) S	EQUE	NCE 1	DESC	RIPT	ION:	SEQ	ID I	NO : 4!	5:				
30	Asp 1	Ile	Val	Met	Thr 5	Gln	Thr	Pro	Leu	Ser 10	Leu	Pro	Val	Ser	Leu 15
35	Gly	Asp	Gln	Ala	Ser 20	Ile	Ser	Суѕ	Arg	Ser 25	Ser	Gln	Ser	Leu	Val 30
33	His	Gly	Ile	Gly	Asn 35	Thr	Tyr	Leu	His	Trp 40	Tyr	Leu	Gln	Lys	Pro 45
40	Gly	Gln	Ser	Pro	Lys 50	Leu	Leu	Ile	Tyr	Туr 55	Lys	Val	Ser	Asn	Arg 60
	Phe	Ser	Gly	Val	Pro 65	Asp	Arg	Phe	Ser	Asp 70	Ser	Gly	Ser	Gly	Thr 75
45	Asp	Phe	Thr	Leu	Arg 80	Ile	Ser	Arg	Val	Glu 85	Ala	Glu	Asp	Leu	Gly 90
50	Leu	Tyr	Phe	Cys	Ser 95	Gln	Ser	Thr	His	Val 100	Pro	Leu	Thr	Phe	Gly 105
-	Ala	Gly	Thr	Lys	Leu 110	Glu	Leu	Lys	Arg 114						
55	, ,					SEQ ACTE	ID N								

		( <i>F</i> (E	3) TY	PE:	Amir	4 am no Ac Line	id	acid	is						
,5	(x:	i) SE	EQUE!	ICE I	DESCF	RIPTI	ON:	SEQ	ID N	10:46	5:				
	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
10	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ser 25	Ser	Gln	Ser	Leu	Val 30
16	His	Gly	Ile	Gly	Asn 35	Thr	Tyr	Leu	His	Trp 40	Туr	Gln	Gln	Lys	Pro 45
15	Gly	Lys	Ala	Pro	Lys 50	Leu	Leu	Ile	Tyr	Tyr 55	Lys	Val	Ser	Asn	Arg 60
20	Phe	Ser	Gly	Val	Pro 65	Ser	Arg	Phe	Ser	Gly 70	Ser	Gly	Ser	Gly	Thr 75
Thur, ma	Asp	Phe	Thr	Leu	Thr 80	Ile	Ser	Ser	Leu	Gln 85	Pro	Glu	Asp	Phe	Ala 90
25	Thr	Tyr	Tyr	Cys	Ser 95	Gln	Ser	Thr	His	Val 100	Pro	Leu	Thr	Phe	Gly 105
thust anne 36.0	Gln	Gly	Thr	Lys	Val 110	Glu	Ile	Lys	Arg 114						
<sup>#</sup> 30	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID N	0:47	:						
1 35	(	(1	A) LI B) T	ENGTI YPE :	H: 10 PRT	ACTE 09 ar Line	mino		ds						
Tandy Fr	(x.	i) S	EQUEI	NCE I	DESCI	RIPT:	ION:	SEQ	ID 1	NO : 4	7:				
40	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	Ser	Val 15
15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Arg	Ala 25	Ser	Lys	Thr	Ile	Ser 30
45	Lys	Tyr	Leu	Ala	Trp 35	Туr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
50	Leu	Leu	Ile	Tyr	Tyr 50	Ser	Gly	Ser	Thr	Leu 55	Glu	Ser	Gly	Val	Pro 60
	Ser	Arg	Phe	Ser	Gly 65	Ser	Gly	Ser	Gly	Thr 70	Asp	Phe	Thr	Leu	Thr 75
55	Ile	Ser	Ser	Leu	Gln 80	Pro	Glu	Asp	Phe	Ala 85	Thr	Tyr	Tyr	Cys	Gln 90
										263					

	Gln	His	Asn	Glu	Tyr 95	Pro	Leu	Thr	Phe	Gly 100	Gln	Gly	Thr	Lys	Val 105
5	Glu	Ile	Lys	Arg 109											
	(2)	INFO	RMATI	ON I	FOR S	SEQ 1	D NO	):48:	:						
10	(:	(1	EQUEN A) LE B) T' C) T(	ength Pe :	H: 11 Amir	17 ar 10 Ac	nino cid		ds						
5	(x:	i) SI	EQUEN	ICE I	DESCE	RIPT	ON:	SEQ	ID 1	NO : 48	3:				
	Glu 1	Ile	Gln	Leu	Gln 5	Gln	Ser	Gly	Pro	Glu 10	Leu	Met	Lys	Pro	Gly 15
20	Ala	Ser	Val	Lys	Ile 20	Ser	Cys	Lys	Ala	Ser 25	Gly	Tyr	Ser	Phe	Ser 30
25	Ser	His	Tyr	Met	His 35	Trp	Val	Lys	Gln	Ser 40	His	Gly	Lys	Ser	Leu 45
	Glu	Trp	Ile	Gly	Туr 50	Ile	Asp	Pro	Ser	Asn 55	Gly	Glu	Thr	Thr	Tyr 60
30	Asn	Gln	Lys	Phe	Lys 65	Gly	Lys	Ala	Thr	Leu 70	Thr	Val	Asp	Thr	Ser 75
	Ser	Ser	Thr	Ala	Asn 80	Val	His	Leu	Ser	Ser 85	Leu	Thr	Ser	Asp	Asp 90
35	Ser	Ala	Val	Tyr	Phe 95	Суѕ	Ala	Ala	Arg	Gly 100	Asp	Tyr	Arg	Tyr	Asn 105
10	Gly	Asp	Trp	Phe	Phe 110	Asp	Val	Trp	Gly	Ala 115	Gly	Thr 117			
ю	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID N	0:49	:						
15	(:	(1	EQUEI A) LI B) T D) T	ENGTI YPE :	H: 1	17 ar	mino cid		ds						
	(x	i) Si	EQUE	NCE 1	DESCI	RIPT	ION:	SEQ	ID I	NO: 49	€:				
50	Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
55	Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Ser	Phe	Ser 30
, ,	Ser	His	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu

					35					40					45
•	Glu	Trp	Val	Gly	Tyr 50	Ile	Asp	Pro	Ser	Asn 55	Gly	Glu	Thr	Thr	Tyr 60
5	Asn	Gln	Lys	Phe	Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75
10	Lys	Asn	Thr	Leu	Туг 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
	Thr	Ala	Val	Tyr	Туг 95	Cys	Ala	Ala	Arg	Gly 100	Asp	Tyr	Arg	Tyr	Asn 105
15	Gly	Asp	Trp	Phe	Phe 110	Asp	Val	Trp	Gly	Gln 115	Gly	Thr 117			
	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:50	:						
20	(:	(1	A) Li B) Ti	ENGTI YPE :	H: 1: PRT	l6 ar	RIST: mino		ds						
		()	D) T	JPOLO	JGY:	Line	ear			•					
25	(x:	i) S	EQUE	NCE I	DESC	RIPT:	ION:	SEQ	ID I	NO:5	0:				
	Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
30	Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Phe	Ser	Phe	Thr 30
35	Gly	His	Trp	Met	Asn 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
.,.,	Glu	Trp	Val	Gly	Met 50	Ile	His	Pro	Ser	Asp 55	Ser	Glu	Thr	Arg	Туr 60
40	Ala	Asp	Ser	Val	Lys 65	Gly	Arg	Phe	Thr	Ile 70	Ser	Arg	Asp	Asn	Ser 75
	Lys	Asn	Thr	Leu	Туr 80	Leu	Gln	Met	Asn	Ser 85	Leu	Arg	Ala	Glu	Asp 90
45	Thr	Ala	Val	Tyr	Туг 95	Суѕ	Ala	Ala	Arg	Gly 100	Ile	Tyr	Phe	Tyr	Gly 105
50	Thr	Thr	Tyr	Phe	Asp 110	Tyr	Trp	Gly	Gln		Thr 116				
	(2)	INFO	RMAT	ION 1	FOR :	SEQ :	ID N	0:51	:						
55	(	()		ENGTI YPE :	H: 2	42 ar			ds						

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

- Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe 5 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser 10 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr 15 Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Ser Arg Phe 20 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser 25 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Ser Thr 110 115 His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 125 130 <sup>§</sup> 30 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp 145 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn 35 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn 175 40 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser 205 45 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly 50 Glu Cys 242
  - 55 (2) INFORMATION FOR SEQ ID NO:52:

the test test

_	(:	(E	4) LE 3) TY	ENGTH		53 an	mino cid		ls						
5	(x:	i) SI	EQUE	VCE I	DESCI	RIPT	ON:	SEQ	ID N	NO : 52	2:				
10	Met 1	Lys	Lys	Asn	Ile 5	Ala	Phe	Leu	Leu	Ala 10	Ser	Met	Phe	Val	Phe 15
10	Ser	Ile	Ala	Thr	Asn 20	Ala	Tyr	Ala	Glu	Val 25	Gln	Leu	Val	Gln	Ser 30
15	Gly	Gly	Gly	Leu	Val 35	Gln	Pro	Gly	Gly	Ser 40	Leu	Arg	Leu	Ser	Cys 45
	Ala	Ala	Ser	Gly	Tyr 50	Ser	Phe	Ser	Ser	His 55	Tyr	Met	His	Trp	Val 60
<b>20</b>	Arg	Gln	Ala	Pro	Gly 65	Lys	Gly	Leu	Glu	Trp 70	Val	Gly	Tyr	Ile	Asp 75
± 25	Pro	Ser	Asn	Gly	Glu 80	Thr	Thr	Tyr	Asn	Gln 85	Lys	Phe	Lys	Gly	Arg 90
. 23	Phe	Thr	Leu	Ser	Arg 95	Asp	Asn	Ser	Lys	Asn 100	Thr	Ala	Tyr	Leu	Gln 105
<sup>1</sup> 30	Met	Asn	Ser	Leu	Arg 110	Ala	Glu	Asp	Thr	Ala 115	Val	Tyr	Tyr	Cys	Ala 120
	Arg	Gly	Asp	Tyr	Arg 125	Tyr	Asn	Gly	Asp	Trp 130	Phe	Phe	Asp	Val	Trp 135
35	Gly	Gln	Gly	Thr	Leu 140	Val	Thr	Val	Ser	Ser 145	Ala	Ser	Thr	Lys	Gly 150
40	Pro	Ser	Val	Phe	Pro 155	Leu	Ala	Pro	Ser	Ser 160	Lys	Ser	Thr	Ser	Gly 165
40	Gly	Thr	Ala	Ala	Leu 170	Gly	Суѕ	Leu	Val	Lys 175	Asp	Tyr	Phe	Pro	Glu 180
45	Pro	Val	Thr	Val	Ser 185	Trp	Asn	Ser	Gly	Ala 190	Leu	Thr	Ser	Gly	Val 195
	His	Thr	Phe	Pro	Ala 200	Val	Leu	Gln	Ser	Ser 205	Gly	Leu	Tyr	Ser	Leu 210
50	Ser	Ser	Val	Val	Thr 215	Val	Pro	Ser	Ser	Ser 220	Leu	Gly	Thr	Gln	Thr 225
55	Tyr	Ile	Суѕ	Asn	Val 230	Asn	His	Lys	Pro	Ser 235	Asn	Thr	Lys	Val	Asp 240
رر	Lys	Lys	Val	Glu	Pro	Lys	Ser	Суѕ	Asp	Lys	Thr	His	Thr		

253

	(2)	INFO	RMAT:	ION I	FOR S	SEQ I	D NO	5:53	:						
5	i)	(1	A) LI B) Ti	ENGTI YPE :	CHARA H: 15 Amir OGY:	59 ar no Ad	nino cid		ls						
10	(xi	i) SI	EQUE	NCE 1	DESCI	RIPT	ON:	SEQ	ID 1	10:53	3:				
	Ser 1	Gly	Gly	Gly	Ser 5	Gly	Ser	Gly	Asp	Phe 10	Asp	Tyr	Glu	Lys	Met 15
15	Ala	Asn	Ala	Asn	Lys 20	Gly	Ala	Met	Thr	Glu 25	Asn	Ala	Asp	Glu	Asn 30
20	Ala	Leu	Gln	Ser	Asp 35	Ala	Lys	Gly	Lys	Leu 40	Asp	Ser	Val	Ala	Thr 45
20	Asp	Tyr	Gly	Ala	Ala 50	Ile	Asp	Gly	Phe	Ile 55	Gly	Asp	Val	Ser	Gly 60
25	Leu	Ala	Asn	Gly	Asn 65	Gly	Ala	Thr	Gly	Asp 70	Phe	Ala	Gly	Ser	Ser 75
	Asn	Ser	Gln	Met	Ala 80	Gln	Val	Gly	Asp	Gly 85	Asp	Asn	Ser	Pro	Leu 90
30	Met	Asn	Asn	Phe	Arg 95	Gln	Tyr	Leu	'Pro	Ser 100	Leu	Pro	Gln	Ser	Val 105
35	Glu	Cys	Arg	Pro	Phe 110	Val	Phe	Ser	Ala	Gly 115	Lys	Pro	Tyr	Glu	Phe 120
55	Ser	Ile	qaA	Cys	Asp 125	Lys	Ile	Asn	Leu	Phe 130	Arg	Gly	Val	Phe	Ala 135
40	Phe	Leu	Leu	Tyr	Val 140	Ala	Thr	Phe	Met	Tyr 145	Val	Phe	Ser	Thr	Phe 150
	Ala	Asn	Ile	Leu	Arg 155	Asn	Lys	Glu	Ser 159						
45	(2)	INFO	RMAT	ION	FOR S	SEQ :	ID NO	0:54	:						
50	(:	() ()	A) L: B) T' C) S'	ENGT: YPE: TRAN	CHARA H: 78 Nucl DEDNI OGY:	80 ba leic ESS:	ase p Acid Sing	pair:	5						
	(x:	i) S	EQUE	NCE :	DESCI	RIPT	ION:	SEQ	ID 1	NO : 5	4:				
55	ATG	AAAA	AGA J	ATAT	CGCA	rt t	CTTC	TTGC	A TC	ratg:	rtcg	TTT	rttc	TAT	50

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	IGCIACAAAC GCATACGCIG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
5	TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA
,	AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACACTGGT ATCAACAGAA 200
	ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
10	CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
	CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
15	ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
15	TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
	GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
20	CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
, ma	CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
<sup>1</sup> / <sub>1</sub> 25	TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
the man	CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
, gran stren	CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
<sup>13</sup> 30	CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780
3 <u>k</u> 3 <u>k</u>	(2) INFORMATION FOR SEQ ID NO:55:
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 253 amino acids
Tardy Anny	(B) TYPE: Amino Acid (D) TOPOLOGY: Linear
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
40	Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe 1 5 10 15
45	Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser 20 25 30
	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys 35 40 45
50	Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val 50 55 60
55	Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp 65 70 75
33	Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg

269

					80					85					90	
e	Phe	Thr	Leu	Ser	Arg 95	Asp	Asn	Ser	Lys	Asn 100	Thr	Ala	Tyr	Leu	Gln 105	
5	Met	Asn	Ser	Leu	Arg 110	Ala	Glu	Asp	Thr	Ala 115	Val	Tyr	Tyr	Cys	Ala 120	
10	Arg	Gly	Asp	Tyr	Arg 125	Tyr	Asn	Gly	Asp	Trp 130	Phe	Phe	Asp	Val	Trp 135	
	Gly	Gln	Gly	Thr	Leu 140	Val	Thr	Val	Ser	Ser 145	Ala	Ser	Thr	Lys	Gly 150	
15	Pro	Ser	Val	Phe	Pro 155	Leu	Ala	Pro	Ser	Ser 160	Lys	Ser	Thr	Ser	Gly 165	
20	Gly	Thr	Ala	Ala	Leu 170	Gly	Cys	Leu	Val	Lys 175	Asp	Tyr	Phe	Pro	Glu 180	
20	Pro	Val	Thr	Val	Ser 185	Trp	Asn	Ser	Gly	Ala 190	Leu	Thr	Ser	Gly	Va1 195	
25	His	Thr	Phe	Pro	Ala 200	Val	Leu	Gln	Ser	Ser 205	Gly	Leu	Tyr	Ser	Leu 210	
	Ser	Ser	Val	Val	Thr 215	Val	Pro	Ser	Ser	Ser 220	Leu	Gly	Thr	Gln	Thr 225	
30	Tyr	Ile	Cys	Asn	Val 230	Asn	His	Lys	Pro	Ser 235	Asn	Thr	Lys	Val	Asp 240	
35	Lys	Lys ·	Val	Glu	Pro 245	Lys	Ser	Суѕ	Asp	Lys 250	Thr	His	Thr 253			
33	(2)	INFO	RMAT:	ION I	FOR :	SEQ	IĎ N	0:56	:							
40	(:	()	EQUEI A) LI B) T' D) T(	ENGT YPE:	H: 24 Amin	42 ai	mino cid		ds							
	(x:	i) S	EQUE	NCE 1	DESC	RIPT	ION:	SEQ	ID I	NO:5	<b>6</b> :					
45	Met 1	Lys	Lys	Asn	Ile 5	Ala	Phe	Leu	Leu	Ala 10		Met	Phe	Val	Phe 15	
50	Ser	Ile	Ala	Thr	Asn 20	Ala	Tyr	Ala	Asp	Ile 25	Gln	Met	Thr	Gln	Ser 30	
20	Pro	Ser	Ser	Leu	Ser 35	Ala	Ser	Val	Gly	Asp 40	Arg	Val	Thr	Ile	Thr 45	
55	Суѕ	Arg	Ser	Ser	Gln 50	Ser	Leu	Val	His	Gly 55	Ile	Gly	Ala	Thr	Tyr 60	

	Leu	His	Trp	Tyr	Gln 65	Gln	Lys	Pro	Gly	Lys 70	Ala	Pro	Lys	Leu	Leu 75
5	Ile	Tyr	Lys	Val	Ser 80	Asn	Arg	Phe	Ser	Gly 85	Val	Pro	Ser	Arg	Phe 90
	Ser	Gly	Ser	Gly	Ser 95	Gly	Thr	Asp	Phe	Thr 100	Leu	Thr	Ile	Ser	Ser 105
10	Leu	Gln	Pro	Glu	Asp 110	Phe	Ala	Thr	Tyr	Tyr 115	Cys	Ser	Gln	Ser	Thr 120
15	His	Val	Pro	Leu	Thr 125	Phe	Gly	Gln	Gly	Thr 130	Lys	Val	Glu	Ile	Lys 135
	Arg	Thr	Val	Ala	Ala 140	Pro	Ser	Val	Phe	Ile 145	Phe	Pro	Pro	Ser	Asp 150
20	Glu	Gln	Leu	Lys	Ser 155	Gly	Thr	Ala	Ser	Val 160	Val	Cys	Leu	Leu	Asn 165
	Asn	Phe	Tyr	Pro	Arg 170	Glu	Ala	Lys	Val	Gln 175	Trp	Lys	Val	Asp	Asn 180
25	Ala	Leu	Gln	Ser	Gly 185	Asn	Ser	Gln	Glu	Ser 190	Val	Thr	Glu	Gln	Asp 195
30	Ser	Lys	Asp	Ser	Thr 200	Tyr	Ser	Leu	Ser	Ser 205	Thr	Leu	Thr	Leu	Ser 210
50	Lys	Ala	Asp	Tyr	Glu 215	Lys	His	Lys	Val	Tyr 220	Ala	Cys	Glu	Val	Thr 225
35	Hiş	Gln	Gly	Leu	Ser 230	Ser	Pro	Val	Thr	Lys 235	Ser	Phe	Asn	Arg	Gly 240
	Glu	Cys 242													
40	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	0:57	<b>:</b> .						
45	(:	(1		ENGTI YPE:	H: 49 Amir	am:			5						
.5	(x:						ION:	SEQ	ID I	NO:57	7:				
							Pro					Gly	Arg	Met	Lys
50	1				5					10					15
	Gln	Leu	Glu	Asp	Lys 20	Val	Glu	Glu	Leu	Leu 25	Ser	Lys	Asn	Tyr	His 30
55	Leu	Glu	Asn	Glu	Val 35	Ala	Arg	Leu	Lys	Lys 40	Leu	Val	Gly	Glu	Arg 45
										271					

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(2) INFORMATION FOR SEQ ID NO:58:									
5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 780 base pairs</li> <li>(B) TYPE: Nucleic Acid</li> <li>(C) STRANDEDNESS: Single</li> <li>(D) TOPOLOGY: Linear</li> </ul>								
0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:								
	ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 50								
15	TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100								
	TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA								
20	AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACACTGGT ATCAACAGAA 200								
	ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250								
	CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300								
25	CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350								
	ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400								
30	TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450								
	GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500								
	CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550								
35	CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600								
	TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650								
40	CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700								
. •	CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750								
	CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780								
45	(2) INFORMATION FOR SEQ ID NO:59:								
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 927 base pairs								

- (B) TYPE: Nucleic Acid
  (C) STRANDEDNESS: Single
  (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

55 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50

		TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG 100
	5	AGGTTCAGCT AGTGCAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150
		CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACTATAT 200
		GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250
	10	TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300
		TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350
	15	CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400
		ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450
		GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500
" dan	20	ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550
Born Aust		TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600
пин нин	25	CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650
114		CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700
nen 'wen		AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750
, ,	30	AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCGTG 800
:: k		CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850
m	35	TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900
11 j		CTCAAAAAGC TTGTCGGGGA GCGCTAA 927
z=#		(2) INFORMATION FOR SEQ ID NO:60:
	40	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 298 amino acids</li></ul>
		(B) TYPE: Amino Acid (D) TOPOLOGY: Linear
	45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
		Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
	50	1 5 10 15
	50	Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser 20 25 30
		Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
	55	35 40 45

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Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val

					50					55					60
5	Arg	Gln	Ala	Pro	Gly 65	Lуs	Gly	Leu	Glu	Trp 70	Val	Gly	Tyr	Ile	Asp 75
J	Pro	Ser	Asn	Gly	Glu 80	Thr	Thr	Tyr	Asn	Gln 85	Lys ,	Phe	Lys	Gly	Arg 90
10	Phe	Thr	Leu	Ser	Arg 95	Asp	Asn	Ser	Lys	Asn 100	Thr	Ala	Tyr	Leu	Gln 105
	Met	Asn	Ser	Leu	Arg 110	Ala	Glu	Asp	Thr	Ala 115	Val	Tyr	Tyr	Суѕ	Ala 120
15	Arg	Gly	Asp	Tyr	Arg 125	Tyr	Asn	Gly	Asp	Trp 130	Phe	Phe	Asp	Val	Trp 135
20	Gly	Gln	Gly	Thr	Leu 140	Val	Thr	Val	Ser	Ser 145	Ala	Ser	Thr	Lys	Gly 150
20	Pro	Ser	Val	Phe	Pro 155	Leu	Ala	Pro	Ser	Ser 160	Lys	Ser	Thr	Ser	Gly 165
[]] []]25	Gly	Thr	Ala	Ala	Leu 170	Gly	Cys	Leu	Val	Lys 175	Asp	Tyr	Phe	Pro	Glu 180
frist med ben	Pro	Val	Thr	Val	Ser 185	Trp	Asn	Ser	Gly	Ala 190	Leu	Thr	Ser	Gly	Val 195
30	His	Thr	Phe	Pro	Ala 200	Val	Leu	Gln	Ser	Ser 205	Gly	Leu	Tyr	Ser	Leu 210
[]] []35	Ser	Ser	Val	Val	Thr 215	Val	Pro	Ser	Ser	Ser 220	Leu	Gly	Thr	Gln	Thr 225
	Tyr	Ile	Суѕ	Asn	Val 230	Asn	His	Lys	Pro	Ser 235	Asn	Thr	Lys	Val	Asp 240
40	Lys	Lys	Val	Glu	Pro 245	Lys	Ser	Cys	Asp	Lys 250	Thr	His	Thr	Cys	Pro 255
	Pro	Суѕ	Pro	Ala	Pro 260	Glu	Leu	Leu	Gly	Gly 265	Arg	Met	Lys	Gln	Leu 270
45	Glu	Asp	Lys	Val	Glu 275	Glu	Leu	Leu	Ser	Lys 280	Asn	Tyr	His	Leu	Glu 285
50	Asn	Glu	Val	Ala	Arg 290	Leu	Lys	Lys	Leu	Val 295	Gly	Glu	Arg 298		
50	(2)	INFO	RMATI	ON F	FOR S	SEQ I	D NO	:61:							

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 6563 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single

#### (D) TOPOLOGY: Linear

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#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAATTCAACT	TCTCCATACT	TTGGATAAGG	AAATACAGAC	ATGAAAAATC	50
TCATTGCTGA	GTTGTTATTT	AAGCTTGCCC	AAAAAGAAGA	AGAGTCGAAT	100
GAACTGTGTG	CGCAGGTAGA	AGCTTTGGAG	ATTATCGTCA	CTGCAATGCT	150
TCGCAATATG	GCGCAAAATG	ACCAACAGCG	GTTGATTGAT	CAGGTAGAGG	200
GGGCGCTGTA	CGAGGTAAAG	CCCGATGCCA	GCATTCCTGA	CGACGATACG	250
GAGCTGCTGC	GCGATTACGT	AAAGAAGTTA	TTGAAGCATC	CTCGTCAGTA	300
AAAAGTTAAT	CTTTTCAACA	GCTGTCATAA	AGTTGTCACG	GCCGAGACTT	350
ATAGTCGCTT	TGTTTTTATT	TTTTAATGTA	TTTGTAACTA	GAATTCGAGC	400
TCGGTACCCG	GGGATCCTCT	CGAGGTTGAG	GTGATTTTAT	GAAAAAGAAT	450
ATCGCATTTC	TTCTTGCATC	TATGTTCGTT	TTTTCTATTG	CTACAAACGC	500
ATACGCTGAT	ATCCAGATGA	CCCAGTCCCC	GAGCTCCCTG	TCCGCCTCTG	550
TGGGCGATAG	GGTCACCATC	ACCTGCAGGT	CAAGTCAAAG	CTTAGTACAT	600
GGTATAGGTG	CTACGTATTT	ACACTGGTAT	CAACAGAAAC	CAGGAAAAGC	650
TCCGAAACTA	CTGATTTACA	AAGTATCCAA	TCGATTCTCT	GGAGTCCCTT	700
CTCGCTTCTC	TGGATCCGGT	TCTGGGACGG	ATTTCACTCT	GACCATCAGC	750
AGTCTGCAGC	CAGAAGACTT	CGCAACTTAT	TACTGTTCAC	AGAGTACTCA	800
TGTCCCGCTC	ACGTTTGGAC	AGGGTACCAA	GGTGGAGATC	AAACGAACTG	850
TGGCTGCACC	ATCTGTCTTC	ATCTTCCCGC	CATCTGATGA	GCAGTTGAAA	900
TCTGGAACTG	CTTCTGTTGT	GTGCCTGCTG	AATAACTTCT	ATCCCAGAGA	950
GGCCAAAGTA	CAGTGGAAGG	TGGATAACGC	CCTCCAATCG	GGTAACTCCC	1000
AGGAGAGTGT	CACAGAGCAG	GACAGCAAGG	ACAGCACCTA	CAGCCTCAGC	1050
AGCACCCTGA	CGCTGAGCAA	AGCAGACTAC	GAGAAACACA	AAGTCTACGC	1100
CTGCGAAGTC	ACCCATCAGG	GCCTGAGCTC	GCCCGTCACA	AAGAGCTTCA	1150
ACAGGGGAGA	GTGTTAAGCT	GATCCTCTAC	GCCGGACGCA	TCGTGGCCCT	1200
AGTACGCAAC	TAGTCGTAAA	AAGGGTATCT	AGAGGTTGAG	GTGATTTTAT	1250
GAAAAAGAAT	ATCGCATTTC	TTCTTGCATC	TATGTTCGTT	TTTTCTATTG	1300

		CTACAAACGC	GTACGCTGAG	GTTCAGCTAG	TGCAGTCTGG	CGGTGGCCTG	1350
	5	GTGCAGCCAG	GGGGCTCACT	CCGTTTGTCC	TGTGCAGCTT	CTGGCTACTC	1400
	J	CTTCTCGAGT	CACTATATGC	ACTGGGTCCG	TCAGGCCCCG	GGTAAGGGCC	1450
		TGGAATGGGT	TGGATATATT	GATCCTTCCA	ATGGTGAAAC	TACGTATAAT	1500
	10	CAAAAGTTCA	AGGGCCGTTT	CACTTTATCT	CGCGACAACT	CCAAAAACAC	1550
		AGCATACCTG	CAGATGAACA	GCCTGCGTGC	TGAGGACACT	GCCGTCTATT	1600
	15	ACTGTGCAAG	AGGGGATTAT	CGCTACAATG	GTGACTGGTT	CTTCGACGTC	1650
	15	TGGGGTCAAG	GAACCCTGGT	CACCGTCTCC	TCGGCCTCCA	CCAAGGGCCC	1700
		ATCGGTCTTC	CCCCTGGCAC	CCTCCTCCAA	GAGCACCTCT	GGGGCACAG	1750
ŧ	20	CGGCCCTGGG	CTGCCTGGTC	AAGGACTACT	TCCCCGAACC	GGTGACGGTG	1800
Trees.		TCGTGGAACT	CAGGCGCCCT	GACCAGCGGC	GTGCACACCT	TCCCGGCTGT	1850
Their Shur	26	CCTACAGTCC	TCAGGACTCT	ACTCCCTCAG	CAGCGTGGTG	ACCGTGCCCT	1900
	25	CCAGCAGCTT	GGGCACCCAG	ACCTACATCT	GCAACGTGAA	TCACAAGCCC	1950
15 Minute		AGCAACACCA	AGGTCGACAA	GAAAGTTGAG	CCCAAATCTT	GTGACAAAAC	2000
,run	30	TCACACATGC	CCGCCGTGCC	CAGCACCAGA	ACTGCTGGGC	GGCCGCATGA	2050
		AACAGCTAGA	GGACAAGGTC	GAAGAGCTAC	TCTCCAAGAA	СТАССАССТА	2100
	25	GAGAATGAAG	TGGCAAGACT	CAAAAAGCTT	GTCGGGGAGC	GCTAAGCATG	2150
1004 1004	35	CGACGGCCCT	AGAGTCCCTA	ACĢCTCGGTT	GCCGCCGGGC	GTTTTTTATT	2200
1111		GTTAACTCAT	GTTTGACAGC	TTATCATCGA	TAAGCTTTAA	TGCGGTAGTT	2250
	40	TATCACAGTT	AAATTGCTAA	CGCAGTCAGG	CACCGTGTAT	GAAATCTAAC	2300
		AATGCGCTCA	TCGTCATCCT	CGGCACCGTC	ACCCTGGATG	CTGTAGGCAT	2350
	45	AGGCTTGGTT	ATGCCGGTAC	TGCCGGGCCT	CTTGCGGGAT	ATCGTCCATT	2400
	40	CCGACAGCAT	CGCCAGTCAC	TATGGCGTGC	TGCTAGCGCT	ATATGCGTTG	2450
		ATGCAATTTC	TATGCGCACC	CGTTCTCGGA	GCACTGTCCG	ACCGCTTTGG	2500
	50	CCGCCGCCCA	GTCCTGCTCG	CTTCGCTACT	TGGAGCCACT	ATCGACTACG	2550
		CGATCATGGC	GACCACACCC	GTCCTGTGGA	TCCTCTACGC	CGGACGCATC	2600
	55	GTGGCCGGCA	TCACCGGCGC	CACAGGTGCG	GTTGCTGGCG	CCTATATCGC	2650
	<b>33</b>	CGACATCACC	GATGGGGAAG	ATCGGGCTCG	CCACTTCGGG	CTCATGAGCG	2700

		CTTGTTTCGG	CGTGGGTATG	GTGGCAGGCC	CCGTGGCCGG	GGGACTGTTG	2750
	5	GGCGCCATCT	CCTTGCACGC	ACCATTCCTT	GCGGCGGCGG	TGCTCAACGG	2800
		CCTCAACCTA	CTACTGGGCT	GCTTCCTAAT	GCAGGAGTCG	CATAAGGGAG	2850
		AGCGTCGTCC	GATGCCCTTG	AGAGCCTTCA	ACCCAGTCAG	CTCCTTCCGG	2900
	10	TGGGCGCGGG	GCATGACTAT	CGTCGCCGCA	CTTATGACTG	TCTTCTTTAT	2950
		CATGCAACTC	GTAGGACAGG	TGCCGGCAGC	GCTCTGGGTC	ATTTTCGGCG	3000
	15	AGGACCGCTT	TCGCTGGAGC	GCGACGATGA	TCGGCCTGTC	GCTTGCGGTA	3050
	13	TTCGGAATCT	TGCACGCCCT	CGCTCAAGCC	TTCGTCACTG	GTCCCGCCAC	3100
		CAAACGTTTC	GGCGAGAAGC	AGGCCATTAT	CGCCGGCATG	GCGGCCGACG	3150
:** <b>1</b>	20	CGCTGGGCTA	CGTCTTGCTG	GCGTTCGCGA	CGCGAGGCTG	GATGGCCTTC	3200
		CCCATTATGA	TTCTTCTCGC	TTCCGGCGGC	ATCGGGATGC	CCGCGTTGCA	3250
# 1 mm	25	GGCCATGCTG	TCCAGGCAGG	TAGATGACGA	CCATCAGGGA	CAGCTTCAAG	3300
der der		GATCGCTCGC	GGCTCTTACC	AGCCTAACTT	CGATCACTGG	ACCGCTGATC	3350
F Han #		GTCACGGCGA	TTTATGCCGC	CTCGGCGAGC	ACATGGAACG	GGTTGGCATG	3400
laij H	30	GATTGTAGGC	GCCGCCCTAT	ACCTTGTCTG	CCTCCCCGCG	TTGCGTCGCG	3450
as b		GTGCATGGAG	CCGGGCCACC	TCGACCTGAA	TGGAAGCCGG	CGGCACCTCG	3500
	35	CTAACGGATT	CACCACTCCA	AGAATTGGAG	CCAATCAATT	CTTGCGGAGA	3550
		ACTGTGAATG	CGCAAACCAA	CCCTTGGCAG	AACATATCCA	TCGCGTCCGC	3600
10.7		CATCTCCAGC	AGCCGCACGC	GGCGCATCTC	GGGCAGCGTT	GGGTCCTGGC	3650
	40	CACGGGTGCG	CATGATCGTG	CTCCTGTCGT	TGAGGACCCG	GCTAGGCTGG	3700
		CGGGGTTGCC	TTACTGGTTA	GCAGAATGAA	TCACCGATAC	GCGAGCGAAC	3750
	45	GTGAAGCGAC	TGCTGCTGCA	AAACGTCTGC	GACCTGAGCA	ACAACATGAA	3800
		TGGTCTTCGG	TTTCCGTGTT	TCGTAAAGTC	TGGAAACGCG	GAAGTCAGCG	3850
		CCCTGCACCA	TTATGTTCCG	GATCTGCATC	GCAGGATGCT	GCTGGCTACC	3900
	50	CTGTGGAACA	CCTACATCTG	TATTAACGAA	GCGCTGGCAT	TGACCCTGAG	3950
		TGATTTTTCT	CTGGTCCCGC	CGCATCCATA	CCGCCAGTTG	TTTACCCTCA	4000
	55	CAACGTTCCA	GTAACCGGGC	ATGTTCATCA	TCAGTAACCC	GTATCGTGAG	4050
		CATCCTCTCT	CGTTTCATCG	GTATCATTAC	CCCCATGAAC	AGAAATTCCC	4100

CCTTACACGG	AGGCATCAAG	TGACCAAACA	GGAAAAAACC	GCCCTTAACA	4150
TGGCCCGCTT	TATCAGAAGC	CAGACATTAA	CGCTTCTGGA	GAAACTCAAC	4200
GAGCTGGACG	CGGATGAACA	GGCAGACATC	TGTGAATCGC	TTCACGACCA	4250
CGCTGATGAG	CTTTACCGCA	GCTGCCTCGC	GCGTTTCGGT	GATGACGGTG	4300
AAAACCTCTG	ACACATGCAG	CTCCCGGAGA	CGGTCACAGC	TTGTCTGTAA	4350
GCGGATGCCG	GGAGCAGACA	AGCCCGTCAG	GGCGCGTCAG	CGGGTGTTGG	4400
CGGGTGTCGG	GGCGCAGCCA	TGACCCAGTC	ACGTAGCGAT	AGCGGAGTGT	4450
ATACTGGCTT	AACTATGCGG	CATCAGAGCA	GATTGTACTG	AGAGTGCACC	4500
ATATGCGGTG	TGAAATACCG	CACAGATGCG	TAAGGAGAAA	ATACCGCATC	4550
AGGCGCTCTT	CCGCTTCCTC	GCTCACTGAC	TCGCTGCGCT	CGGTCGTTCG	4600
GCTGCGGCGA	GCGGTATCAG	CTCACTCAAA	GGCGGTAATA	CGGTTATCCA	4650
CAGAATCAGG	GGATAACGCA	GGAAAGAACA	TGTGAGCAAA	AGGCCAGCAA	4700
AAGGCCAGGA	ACCGTAAAAA	GGCCGCGTTG	CTGGCGTTTT	TCCATAGGCT	4750
CCGCCCCCCT	GACGAGCATC	ACAAAAATCG	ACGCTCAAGT	CAGAGGTGGC	4800
GAAACCCGAC	AGGACTATAA	AGATACCAGG	CGTTTCCCCC	TGGAAGCTCC	4850
CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	CTTACCGGAT	ACCTGTCCGC	4900
CTTTCTCCCT	TCGGGAAGCG	TGGCGCTTTC	TCATAGCTCA	CGCTGTAGGT	4950
ATCTCAGTTC	GGTGTAGGTC	GTTCGCTCCA	AGCTGGGCTG	TGTGCACGAA	5000
CCCCCGTTC	AGCCCGACCG	CTGCGCCTTA	TCCGGTAACT	ATCGTCTTGA	5050
GTCCAACCCG	GTAAGACACG	ACTTATCGCC	ACTGGCAGCA	GCCACTGGTA	5100
ACAGGATTAG	CAGAGCGAGG	TATGTAGGCG	GTGCTACAGA	GTTCTTGAAG	5150
TGGTGGCCTA	ACTACGGCTA	CACTAGAAGG	ACAGTATTTG	GTATCTGCGC	5200
TCTGCTGAAG	CCAGTTACCT	TCGGAAAAAG	AGTTGGTAGC	TCTTGATCCG	5250
GCAAACAAAC	CACCGCTGGT	AGCGGTGGTT	TTTTTGTTTG	CAAGCAGCAG	5300
ATTACGCGCA	GAAAAAAAGG	ATCTCAAGAA	GATCCTTTGA	TCTTTTCTAC	5350
GGGGTCTGAC	GCTCAGTGGA	ACGAAAACTC	ACGTTAAGGG	ATTTTGGTCA	5400
TGAGATTATC	AAAAAGGATC	TTCACCTAGA	ТССТТТТААА	TTAAAAATGA	5450
AGTTTTAAAT	CAATCTAAAG	TATATATGAG	TAAACTTGGT	CTGACAGTTA	5500

72 L

25 min 2 min

CCAATGCTTA	ATCAGTGAGG	CACCTATCTC	AGCGATCTGT	CTATTTCGTT	5550
CATCCATAGT	TGCCTGACTC	CCCGTCGTGT	AGATAACTAC	GATACGGGAG	5600
GGCTTACCAT	CTGGCCCCAG	TGCTGCAATG	ATACCGCGAG	ACCCACGCTC	5650
ACCGGCTCCA	GATTTATCAG	СААТАААССА	GCCAGCCGGA	AGGGCCGAGC	5700
GCAGAAGTGG	TCCTGCAACT	TTATCCGCCT	CCATCCAGTC	TATTAATTGT	5750
TGCCGGGAAG	CTAGAGTAAG	TAGTTCGCCA	GTTAATAGTT	TGCGCAACGT	5800
TGTTGCCATT	GCTGCAGGCA	TCGTGGTGTC	ACGCTCGTCG	TTTGGTATGG	5850
CTTCATTCAG	CTCCGGTTCC	CAACGATCAA	GGCGAGTTAC	ATGATCCCCC	5900
ATGTTGTGCA	AAAAAGCGGT	TAGCTCCTTC	GGTCCTCCGA	TCGTTGTCAG	5950
AAGTAAGTTG	GCCGCAGTGT	TATCACTCAT	GGTTATGGCA	GCACTGCATA	6000
ATTCTCTTAC	TGTCATGCCA	TCCGTAAGAT	GCTTTTCTGT	GACTGGTGAG	6050
TACTCAACCA	AGTCATTCTG	AGAATAGTGT	ATGCGGCGAC	CGAGTTGCTC	6100
TTGCCCGGCG	TCAACACGGG	ATAATACCGC	GCCACATAGC	AGAACTTTAA	6150
AAGTGCTCAT	CATTGGAAAA	CGTTCTTCGG	GGCGAAAACT	CTCAAGGATC	6200
TTACCGCTGT	TGAGATCCAG	TTCGATGTAA	CCCACTCGTG	CACCCAACTG	6250
ATCTTCAGCA	TCTTTTACTT	TCACCAGCGT	TTCTGGGTGA	GCAAAAACAG	6300
GAAGGCAAAA	TGCCGCAAAA	AAGGGAATAA	GGGCGACACG	GAAATGTTGA	6350
ATACTCATAC	TCTTCCTTTT	TCAATATTAT	TGAAGCATTT	ATCAGGGTTA	6400
TTGTCTCATG	AGCGGATACA	TATTTGAATG	TATTTAGAAA	AATAAACAAA	6450
TAGGGGTTCC	GCGCACATTT	CCCCGAAAAG	TGCCACCTGA	CGTCTAAGAA	6500
ACCATTATTA	TCATGACATT	AACCTATAAA	AATAGGCGTA	TCACGAGGCC	6550
CTTTCGTCTT	CAA 6563				

(2) INFORMATION FOR SEQ ID NO:62:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 242 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
- 55 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe 1 5 10 15

	Ser	Ile	Ala	Thr	Asn 20	Ala	Tyr	Ala	Asp	Ile 25	Gln	Met	Thr	Gln	Ser 30
5	Pro	Ser	Ser	Leu	Ser 35	Ala	Ser	Val	Gly	Asp 40	Arg	Val	Thr	Ile	Thr 45
10	Cys	Arg	Ser	Ser	Gln 50	Ser	Leu	Val	His	Gly 55	Ile	Gly	Glu	Thr	<b>Tyr</b> 60
10	Leu	His	Trp	Tyr	Gln 65	Gln	Lys	Pro	Gly	Lys 70	Ala	Pro	Lys	Leu	Leu 75
15	Ile	Tyr	Lys	Val	Ser 80	Asn	Arg	Phe	Ser	Gly 85	Val	Pro	Ser	Arg	Phe 90
	Ser	Gly	Ser	Gly	Ser 95	Gly	Thr	Asp	Phe	Thr 100	Leu	Thr	Ile	Ser	Ser 105
20	Leu	Gln	Pro	Glu	Asp 110	Phe	Ala	Thr	Tyr	Туг 115	Суѕ	Ser	Gln	Ser	Thr 120
26	His	Val	Pro	Leu	Thr 125	Phe	Gly	Gln	Gly	Thr 130	Lys	Val	Glu	Ile	Lys 135
25	Arg	Thr	Val	Ala	Ala 140	Pro	Ser	Val	Phe	Ile 145	Phe	Pro	Pro	Ser	Asp 150
30	Glu	Gln	Leu	Lys	Ser 155	Gly	Thr	Ala	Ser	Val 160	Val	Cys	Leu	Leu	Asr 165
; ;	Asn	Phe	Tyr	Pro	Arg 170	Glu	Ala	Lys	Val	Gln 175	Trp	Lys	Val	Asp	Asr 180
35	Ala	Leu	Gln	Ser	Gly 185	Asn	Ser	Gln	Glu	Ser 190	Val	Thr	Glu	Gln	Asp 195
40	Ser	Lys	Asp	Ser	Thr 200	Tyr	Ser	Leu	Ser	Ser 205	Thr	Leu	Thr	Leu	Ser 210
40	Lys	Ala	Asp	Tyr	Glu 215	Lys	His	Lys	Val	Tyr 220	Ala	Cys	Glu	Val	Thr 225
45	His	Gln	Gly	Leu	Ser 230	Ser	Pro	Val	Thr	Lys 235	Ser	Phe	Asn	Arg	Gly 240
	Glu	Cys 242													

50 (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
    (B) TYPE: Nucleic Acid
    (C) STRANDEDNESS: Single
    (D) TOPOLOGY: Linear

		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
	5	CATGGTATAG GTTAAACTTA TTTACAC 27	
		(2) INFORMATION FOR SEQ ID NO:64:	
	10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 27 base pairs</li> <li>(B) TYPE: Nucleic Acid</li> <li>(C) STRANDEDNESS: Single</li> <li>(D) TOPOLOGY: Linear</li> </ul>	
	15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
		CATGGTATAG GTNNSACTTA TTTACAC 27	
	20	(2) INFORMATION FOR SEQ ID NO:65:	
freit, anne mit gene it gene in finnt freit	25	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 780 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Single</li><li>(D) TOPOLOGY: Linear</li></ul>	,
L. Land Chang L.	30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
18 1.		ATGAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTTTCTAT 5	
		TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 1	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	35	TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA	
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		AGCTTAGTAC ATGGTATAGG TGAGACGTAT TTACACTGGT ATCAACAGAA 2	
	40	ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 2	
		CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 3  CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 3	
	15	ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 4	
	45	TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 4	
		GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 5	
	50	CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT	
		CIAICCIANA GAUGCCIANA IACAGIGGAA GGIGGAIAAC GCCCICCAAI	

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TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650

	CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
	CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
5	CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780
	(2) INFORMATION FOR SEQ ID NO:66:
10	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 78 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Single</li><li>(D) TOPOLOGY: Linear</li></ul>
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
	CTAGTGCAGT CTGGCGGTGG CCTGGTGCAG CCAGGGGGCT CACTCCGTTT 50
20	GTCCTGTGCA GCTTCTGGCT ACTCCTTC 78
a a accession of the state of t	(2) INFORMATION FOR SEQ ID NO:67:
eng mer	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 82 base pairs</li><li>(B) TYPE: Nucleic Acid</li><li>(C) STRANDEDNESS: Single</li><li>(D) TOPOLOGY: Linear</li></ul>
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
41 h	TCGAGAAGGA GTAGCCAGAA GCTGCACAGG ACAAACGGAG TGAGCCCCCT 50
35	GGCTGCACCA GGCCACCGCC AGACTGCACT AG 82
	(2) INFORMATION FOR SEQ ID NO:68:
40	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 8120 base pairs</li> <li>(B) TYPE: Nucleic Acid</li> <li>(C) STRANDEDNESS: Single</li> <li>(D) TOPOLOGY: Linear</li> </ul>
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
	TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG 50
50	GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 100
	GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 150
55	TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 200
	GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 250

CGCCCAGTTC	CGCCCATTCT	CCGCCCCATG	GCTGACTAAT	TTTTTTTTTT	300
TATGCAGAGG	CCGAGGCCGC	CTCGGCCTCT	GAGCTATTCC	AGAAGTAGTG	350
AGGAGGCTTT	TTTGGAGGCC	TAGGCTTTTG	CAAAAAGCTA	GCTTATCCGG	400
CCGGGAACGG	TGCATTGGAA	CGCGGATTCC	CCGTGCCAAG	AGTGACGTAA	450
GTACCGCCTA	TAGAGCGATA	AGAGGATTTT	ATCCCCGCTG	CCATCATGGT	500
TCGACCATTG	AACTGCATCG	TCGCCGTGTC	CCAAAATATG	GGGATTGGCA	550
AGAACGGAGA	CCTACCCTGG	CCTCCGCTCA	GGAACGAGTT	CAAGTACTTC	600
CAAAGAATGA	CCACAACCTC	TTCAGTGGAA	GGTAAACAGA	ATCTGGTGAT	650
TATGGGTAGG	AAAACCTGGT	TCTCCATTCC	TGAGAAGAAT	CGACCTTTAA	700
AGGACAGAAT	TAATATAGTT	CTCAGTAGAG	AACTCAAAGA	ACCACCACGA	750
GGAGCTCATT	TTCTTGCCAA	AAGTTTGGAT	GATGCCTTAA	GACTTATTGA	800
ACAACCGGAA	TTGGCAAGTA	AAGTAGACAT	GGTTTGGATA	GTCGGAGGCA	850
GTTCTGTTTA	CCAGGAAGCC	ATGAATCAAC	CAGGCCACCT	TAGACTCTTT	900
GTGACAAGGA	TCATGCAGGA	ATTTGAAAGT	GACACGTTTT	TCCCAGAAAT	950
TGATTTGGGG	AAATATAAAC	CTCTCCCAGA	ATACCCAGGC	GTCCTCTCTG	1000
AGGTCCAGGA	GGAAAAAGGC	ATCAAGTATA	AGTTTGAAGT	CTACGAGAAG	1050
AAAGACTAAC	AGGAAGATGC	TTTCAAGTTC	TCTGCTCCCC	TCCTAAAGCT	1100
ATGCATTTTT	ATAAGACCAT	GGGACTTTTG	CTGGCTTTAG	ATCCCCTTGG	1150
CTTCGTTAGA	ACGCAGCTAC	AATTAATACA	TAACCTTATG	TATCATACAC	1200
ATACGATTTA	GGTGACACTA	TAGATAACAT	CCACTTTGCC	TTTCTCTCCA	1250
CAGGTGTCCA	CTCCCAGGTC	CAACTGCACC	TCGGTTCTAT	CGATTGAATT	1300
CCACCATGGG	ATGGTCATGT	ATCATCCTTT	TTCTAGTAGC	AACTGCAACT	1350
GGAGTACATT	CAGAAGTTCA	GCTAGTGCAG	TCTGGCGGTG	GCCTGGTGCA	1400
GCCAGGGGGC	TCACTCCGTT	TGTCCTGTGC	AGCTTCTGGC	TACTCCTTCT	1450
CGAGTCACTA	TATGCACTGG	GTCCGTCAGG	CCCCGGGTAA	GGGCCTGGAA	1500
TGGGTTGGAT	ATATTGATCC	TTCCAATGGT	GAAACTACGT	АТААТСАААА	1550
GTTCAAGGGC	CGTTTCACTT	TATCTCGCGA	CAACTCCAAA	AACACAGCAT	1600
ACCTGCAGAT	GAACAGCCTG	CGTGCTGAGG	ACACTGCCGT	CTATTACTGT	1650

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30 and a second production of the second produ

		GCAAGAGGGG	ATTATCGCTA	CAATGGTGAC	TGGTTCTTCG	ACGTCTGGGG	1700
	_	TCAAGGAACC	CTGGTCACCG	TCTCCTCGGC	CTCCACCAAG	GGCCCATCGG	1750
	5	TCTTCCCCCT	GGCACCCTCC	TCCAAGAGCA	CCTCTGGGGG	CACAGCGGCC	1800
		CTGGGCTGCC	TGGTCAAGGA	CTACTTCCCC	GAACCGGTGA	CGGTGTCGTG	1850
	10	GAACTCAGGC	GCCCTGACCA	GCGGCGTGCA	CACCTTCCCG	GCTGTCCTAC	1900
		AGTCCTCAGG	ACTCTACTCC	CTCAGCAGCG	TGGTGACTGT	GCCCTCTAGC	1950
	15	AGCTTGGGCA	CCCAGACCTA	CATCTGCAAC	GTGAATCACA	AGCCCAGCAA	2000
	13	CACCAAGGTG	GACAAGAAAG	TTGAGCCCAA	ATCTTGTGAC	AAAACTCACA	2050
		CATGCCCACC	GTGCCCAGCA	CCTGAACTCC	TGGGGGGACC	GTCAGTCTTC	2100
	20	CTCTTCCCCC	CAAAACCCAA	GGACACCCTC	ATGATCTCCC	GGACCCCTGA	2150
n dend Ann		GGTCACATGC	GTGGTGGTGG	ACGTGAGCCA	CGAAGACCCT	GAGGTCAAGT	2200
tura Benu	25	TCAACTGGTA	CGTGGACGGC	GTGGAGGTGC	ATÄATGCCAA	GACAAAGCCG	2250
from conf three	23	CGGGAGGAGC	AGTACAACAG	CACGTACCGT	GTGGTCAGCG	TCCTCACCGT	2300
1		CCTGCACCAG	GACTGGCTGA	ATGGCAAGGA	GTACAAGTGC	AAGGTCTCCA	2350
, t	30	ACAAAGCCCT	CCCAGCCCCC	ATCGAGAAAA	CCATCTCCAA	AGCCAAAGGG	2400
: h		CAGCCCCGAG	AACCACAGGT	GTACACCCTG	CCCCCATCCC	GGGAAGAGAT	2450
THE STATE OF	35	GACÇAAGAAC	CAGGTCAGCC	TGACCTGCCT	GGTCAAAGGC	TTCTATCCCA	2500
Therefore	<i></i>	GCGACATCGC	CGTGGAGTGG	GAGAGCAATG	GGCAGCCGGA	GAACAACTAC	2550
4,111		AAGACCACGC	CTCCCGTGCT	GGACTCCGAC	GGCTCCTTCT	TCCTCTACAG	2600
	40	CAAGCTCACC	GTGGACAAGA	GCAGGTGGCA	GCAGGGGAAC	GTCTTCTCAT	2650
		GCTCCGTGAT	GCATGAGGCT	CTGCACAACC	ACTACACGCA	GAAGAGCCTC	2700
	45	TCCCTGTCTC	CGGGTAAATG	AGTGCGACGG	CCCTAGAGTC	GACCTGCAGA	2750
		AGCTTGGCCG	CCATGGCCCA	ACTTGTTTAT	TGCAGCTTAT	AATGGTTACA	2800
		AATAAAGCAA	TAGCATCACA	AATTTCACAA	ATAAAGCATT	TTTTTCACTG	2850
:	50	CATTCTAGTT	GTGGTTTGTC	CAAACTCATC	AATGTATCTT	ATCATGTCTG	2900
		GATCGATCGG	GAATTAATTC	GGCGCAGCAC	CATGGCCTGA	AATAACCTCT	2950
	55	GAAAGAGGAA	CTTGGTTAGG	TACCTTCTGA	GGCGGAAAGA	ACCATCTGTG	3000
•		GAATGTGTGT	CAGTTAGGGT	GTGGAAAGTC	CCCAGGCTCC	CCAGCAGGCA	3050

	GAAGTATGCA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAG	GTGTGGAAAG	3,100
5	TCCCCAGGCT	CCCCAGCAGG	CAGAAGTATG	CAAAGCATGC	ATCTCAATTA	3150
3	GTCAGCAACC	ATAGTCCCGC	CCCTAACTCC	GCCCATCCCG	CCCCTAACTC	3200
	CGCCCAGTTC	CGCCCATTCT	CCGCCCCATG	GCTGACTAAT	TTTTTTTTTTT	3250
10	TATGCAGAGG	CCGAGGCCGC	CTCGGCCTCT	GAGCTATTCC	AGAAGTAGTG	3300
	AGGAGGCTTT	TTTGGAGGCC	TAGGCTTTTG	CAAAAAGCTA	GCTTATCCGG	3350
15	CCGGGAACGG	TGCATTGGAA	CGCGGATTCC	CCGTGCCAAG	AGTCAGGTAA	3400
15	GTACCGCCTA	TAGAGTCTAT	AGGCCCACCC	CCTTGGCTTC	GTTAGAACGC	3450
	GGCTACAATT	AATACATAAC	CTTTTGGATC	GATCCTACTG	ACACTGACAT	3500
20	CCACTTTTTC	TTTTTCTCCA	CAGGTGTCCA	CTCCCAGGTC	CAACTGCACC	3550
	TCGGTTCGCG	AAGCTAGCTT	GGGCTGCATC	GATTGAATTC	CACCATGGGA	3600
25	TGGTCATGTA	TCATCCTTTT	TCTAGTAGCA	ACTGCAACTG	GAGTACATTC	3650
23	AGATATCCAG	ATGACCCAGT	CCCCGAGCTC	CCTGTCCGCC	TCTGTGGGCG	3700
	ATAGGGTCAC	CATCACCTGC	AGGTCAAGTC	AAAGCTTAGT	ACATGGTATA	3750
30	GGTGCTACGT	ATTTACACTG	GTATCAACAG	AAACCAGGAA	AAGCTCCGAA	3800
	ACTACTGATT	TACAAAGTAT	CCAATCGATT	CTCTGGAGTC	CCTTCTCGCT	3850
35	TCTCTGGATC	CGGTTCTGGG	ACGGATTTCA	CTCTGACCAT	CAGCAGTCTG	3900
33	CAGCCAGAAG	ACTTCGCAAC	TTATTACTGT	TCACAGAGTA	CTCATGTCCC	3950
	GCTCACGTTT	GGACAGGGTA	CCAAGGTGGA	GATCAAACGA	ACTGTGGCTG	4000
40	CACCATCTGT	CTTCATCTTC	CCGCCATCTG	ATGAGCAGTT	GAAATCTGGA	4050
	ACTGCTTCTG	TTGTGTGCCT	GCTGAATAAC	TTCTATCCCA	GAGAGGCCAA	4100
45	AGTACAGTGG	AAGGTGGATA	ACGCCCTCCA	ATCGGGTAAC	TCCCAGGAGA	4150
1.5	GTGTCACAGA	GCAGGACAGC	AAGGACAGCA	CCTACAGCCT	CAGCAGCACC	4200
	CTGACGCTGA	GCAAAGCAGA	CTACGAGAAA	CACAAAGTCT	ACGCCTGCGA	4250
50	AGTCACCCAT	CAGGGCCTGA	GCTCGCCCGT	CACAAAGAGC	TTCAACAGGG	4300
	GAGAGTGTTA	AGCTTGGCCG	CCATGGCCCA	ACTTGTTTAT	TGCAGCTTAT	4350
55	AATGGTTACA	AATAAAGCAA	TAGCATCACA	AATTTCACAA	ATAAAGCATT	4400
55	TTTTTCACTG	CATTCTAGTT	GTGGTTTGTC	CAAACTCATC	AATGTATCTT	4450

	ATCATGTCTG	GATCGATCGG	GAATTAATTC	GGCGCAGCAC	CATGGCCTGA	4500
	AATAACCTCT	GAAAGAGGAA	CTTGGTTAGG	TACCTTCTGA	GGCGGAAAGA	4550
	ACCAGCTGTG	GAATGTGTGT	CAGTTAGGGT	GTGGAAAGTC	CCCAGGCTCC	4600
	CCAGCAGGCA	GAAGTATGCA	AAGCATGCAT	CTCAATTAGT	CAGCAACCAG	4650
	GTGTGGAAAG	TCCCCAGGCT	CCCCAGCAGG	CAGAAGTATG	CAAAGCATGC	4700
	ATCTCAATTA	GTCAGCAACC	ATAGTCCCGC	CCCTAACTCC	GCCCATCCCG	4750
	CCCCTAACTC	CGCCCAGTTC	CGCCCATTCT	CCGCCCCATG	GCTGACTAAT	4800
	TTTTTTTTT	TATGCAGAGG	CCGAGGCCGC	CTCGGCCTCT	GAGCTATTCC	4850
	AGAAGTAGTG	AGGAGGCTTT	TTTGGAGGCC	TAGGCTTTTG	CAAAAAGCTG	4900
1	TTACCTCGAG	CGGCCGCTTA	ATTAAGGCGC	GCCATTTAAA	TCCTGCAGGT	4950
	AACAGCTTGG	CACTGGCCGT	CGTTTTACAA	CGTCGTGACT	GGGAAAACCC	5000
	TGGCGTTACC	CAACTTAATC	GCCTTGCAGC	ACATCCCCC	TTCGCCAGCT	5050
	GGCGTAATAG	CGAAGAGGCC	CGCACCGATC	GCCCTTCCCA	ACAGTTGCGT	5100
	AGCCTGAATG	GCGAATGGCG	CCTGATGCGG	TATTTTCTCC	TTACGCATCT	5150
•	GTGCGGTATT	TCACACCGCA	TACGTCAAAG	CAACCATAGT	ACGCGCCC.TG	5200
	TAGCGGCGCA	TTAAGCGCGG	CGGGTGTGGT	GGTTACGCGC	AGCGTGACCG	5250
	CTACACTTGC	CAGCGCCCTA	GCGCCCGCTC	CTTTCGCTTT	CTTCCCTTCC	5300
	TTTCTCGCCA	CGTTCGCCGG	CTTTCCCCGT	CAAGCTCTAA	ATCGGGGGCT	5350
	CCCTTTAGGG	TTCCGATTTA	GTGCTTTACG	GCACCTCGAC	CCCAAAAAAC	5400
)	TTGATTTGGG	TGATGGTTCA	CGTAGTGGGC	CATCGCCCTG	ATAGACGGTT	5450
	TTTCGCCCTT	TGACGTTGGA	GTCCACGTTC	TTTAATAGTG	GACTCTTGTT	5500
	CCAAACTGGA	ACAACACTCA	ACCCTATCTC	GGGCTATTCT	TTTGATTTAT	5550
	AAGGGATTTT	GCCGATTTCG	GCCTATTGGT	TAAAAAATGA	GCTGATTTAA	5600
	САААААТТТА	ACGCGAATTT	TAACAAAATA	TTAACGTTTA	CAATTTTATG	5650
)	GTGCACTCTC	AGTACAATCT	GCTCTGATGC	CGCATAGTTA	AGCCAACTCC	5700
	GCTATCGCTA	CGTGACTGGG	TCATGGCTGC	GCCCCGACAC	CCGCCAACAC	5750
	CCGCTGACGC	GCCCTGACGG	GCTTGTCTGC	TCCCGGCATC	CGCTTACAGA	5800
	CAAGCTGTGA	CCGTCTCCGG	GAGCTGCATG	TGTCAGAGGT	TTTCACCGTC	5850

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ATCACCGAAA	CGCGCGAGGC	AGTATTCTTG	AAGACGAAAG	GGCCTCGTGA	5900
TACGCCTATT	TTTATAGGTT	AATGTCATGA	TAATAATGGT	TTCTTAGACG	5950
TCAGGTGGCA	CTTTTCGGGG	AAATGTGCGC	GGAACCCCTA	TTTGTTTATT	6000
ТТТСТАААТА	CATTCAAATA	TGTATCCGCT	CATGAGACAA	TAACCCTGAT	6050
AAATGCTTCA	ATAATATTGA	AAAAGGAAGA	GTATGAGTAT	TCAACATTTC	6100
CGTGTCGCCC	TTATTCCCTT	TTTTGCGGCA	TTTTGCCTTC	CTGTTTTTGC	6150
TCACCCAGAA	ACGCTGGTGA	AAGTAAAAGA	TGCTGAAGAT	CAGTTGGGTG	6200
CACGAGTGGG	TTACATCGAA	CTGGATCTCA	ACAGCGGTAA	GATCCTTGAG	6250
AGTTTTCGCC	CCGAAGAACG	TTTTCCAATG	ATGAGCACTT	TTAAAGTTCT	6300
GCTATGTGGC	GCGGTATTAT	CCCGTGATGA	CGCCGGGCAA	GAGCAACTCG	6350
GTCGCCGCAT	ACACTATTCT	CAGAATGACT	TGGTTGAGTA	CTCACCAGTC	6400
ACAGAAAAGC	ATCTTACGGA	TGGCATGACA	GTAAGAGAAT	TATGCAGTGC	6450
TGCCATAACC	ATGAGTGATA	ACACTGCGGC	CAACTTACTT	CTGACAACGA	6,500
TCGGAGGACC	GAAGGAGCTA	ACCGCTTTTT	TGCACAACAT	GGGGGATCAT	6550
GTAACTCGCC	TTGATCGTTG	GGAACCGGAG	CTGAATGAAG	CCATACCAAA	6600
CGACGAGCGT	GACACCACGA	TGCCAGCAGC	AATGGCAACA	ACGTTGCGCA	6650
AACTATTAAC	TGGCGAACTA	CTTACTCTAG	CTTCCCGGCA	ACAATTAATA	6700
GACTGGATGG	AGGCGGATAA	AGTTGCAGGA	CCACTTCTGC	GCTCGGCCCT	6750
TCCGGCTGGC	TGGTTTATTG	CTGATAAATC	TGGAGCCGGT	GAGCGTGGGT	6800
CTCGCGGTAT	CATTGCAGCA	CTGGGGCCAG	ATGGTAAGCC	CTCCCGTATC	6850
GTAGTTATCT	ACACGACGGG	GAGTCAGGCA	ACTATGGATG	AACGAAATAG	6900
ACAGATCGCT	GAGATAGGTG	CCTCACTGAT	TAAGCATTGG	TAACTGTCAG	6950
ACCAAGTTTA	СТСАТАТАТА	CTTTAGATTG	ATTTAAAACT	TCATTTTTAA	7000
TTTAAAAGGA	TCTAGGTGAA	GATCCTTTTT	GATAATCTCA	TGACCAAAAT	7050
CCCTTAACGT	GAGTTTTCGT	TCCACTGAGC	GTCAGACCCC	GTAGAAAAGA	7100
TCAAAGGATC	TTCTTGAGAT	CCTTTTTTTC	TGCGCGTAAT	CTGCTGCTTG	7150
САААСААААА	AACCACCGCT	ACCAGCGGTG	GTTTGTTTGC	CGGATCAAGA	7200
GCTACCAACT	CTTTTTCCGA	AGGTAACTGG	CTTCAGCAGA	GCGCAGATAC	7250

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CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC 7300 TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 7350 TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT 7400 AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA 7450 10 CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG 7500 TGAGCATTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT 7550 ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA 7600 15 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 7650 ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA 7700 20 AAAACGCCAG CAACGCGGCC TTTTTACGGT TCCTGGCCTT TTGCTGGCCT 7750 TTTGCTCACA TGTTCTTTCC TGCGTTATCC CCTGATTCTG TGGATAACCG 7800 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCAGC CGAACGACCG 7850 125 AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA 7900 CCGCCTCTCC CCGCGCGTTG GCCGATTCAT TAATCCAGCT GGCACGACAG 7950 30 GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT 8000 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT 8050 ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA 8100 ....35 TGACCATGAT TACGAATTAA 8120

- (2) INFORMATION FOR SEQ ID NO:69:
- 40 (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 800 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
- AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50 50 TCTTCTTGCA TCTATGTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG 100 AGGTTCAGCT AGTGCAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150 55 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACTATAT 200

# 

	GCA	CTGGG	STC (	CGTCA	AGGCC	c co	GGTA	AGGG	CCI	GGA	ATGG	GTT	GATA	ATA	250
	TTG	ATCCI	TTC (	CAATO	GTGA	A A	CTACC	TATA	ATC	AAA:	GTT	CAAC	GGCC	CGT	300
5	TTC	ACTTI	TAT (	CTCGC	GACA	A CI	CCA	\AAAC	AC#	AGCAT	TACC	TGC	AGATO	SAA	350
	CAG	CTG	CGT (	GCTG2	AGGAC	CA CT	rgccc	STCTA	TT	CTG	rgca	AGAC	GGG/	ATT	400
10	ATC	GCTAC	CAA T	rggto	GACTO	G T	rcttc	GAC	TCI	rggg	STCA	AGGA	AACC	CTG	450
10	GTC	ACCGI	CT (	CCTCC	GCCI	rc ca	ACCA!	AGGGC	CCI	ATCGO	STCT	TCC	CCT	GGC	500
	ACC	CTCCI	rcc A	AAGAC	CACC	er ca	rggg	GCAC	: AGC	CGGC	CTG	GGC	rgcci	rgg	550
15	TCA	AGGAC	CTA (	CTTCC	CCGA	AA CO	CGGT	GACGO	TG	rcgro	GGAA	CTC	AGGC	GCC	600
	CTG	ACCAC	GCG (	SCGTO	CACA	AC CT	rtcco	CGGCT	GT(	CTAC	CAGT	CCT	CAGG	ACT	650
20	CTAC	CTCCC	CTC A	AGCAC	CGTC	G TO	GACCO	STGC	CTO	CCAG	CAGC	TTG	GCA	CCC	700
-0	AGA	CCTAC	CAT (	CTGC	AACGI	rg az	ATCAC	CAAGO	CCA	AGCA	ACAC	CAA	GTC	GAC	750
	AAG	AAAGI	TTG 1	AGCC	CAAAC	rc T	rgtga	ACAA	A AC	rcaci	ACAT	GCC	GCC'	<b>TGA</b>	800
25	(2)	INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	70:70							
	(:	•	_	NCE (					ls						
30		( 1	3) T	YPE: OPOLO	Amir	no A	cid								
	(x.	i) SI	EQUEI	NCE I	DESCI	RIPT:	ION:	SEQ	ID I	NO : 70	0:				
35	Meţ 1	Lys	Lys	Asn	Ile 5	Ala	Phe	Leu	Leu	Ala 10	Ser	Met	Phe	Val	Phe 15
	Ser	Ile	Ala	Thr	Asn 20	Ala	Tyr	Ala	Glu	Val 25	Gln	Leu	Val	Gln	Ser 30
40	Gly	Gly	Gly	Leu	Val 35	Gln	Pro	Gly	Gly	Ser 40	Leu	Arg	Leu	Ser	Cys 45
45	Ala	Ala	Ser	Gly	Tyr 50	Ser	Phe	Ser	Ser	His 55	Tyr	Met	His	Trp	Val 60
	Arg	Gln	Ala	Pro	Gly 65	Lys	Gly	Leu	Glu	Trp 70	Val	Gly	Tyr	Ile	Asp 75
50	Pro	Ser	Asn	Gly	Glu 80	Thr	Thr	Tyr	Asn	Gln 85	Lys	Phe	Lys	Gly	Arg 90
	Phe	Thr	Leu	Ser	Arg 95	Asp	Asn	Ser	Lys	Asn 100	Thr	Ala	Tyr	Leu	Gln 105
55	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala



	Arg	Gly	Asp	Tyr	Arg 125	Tyr	Asn	Gly	Asp	Trp 130	Phe	Phe	Asp	Val	Trp 135
5	Gly	Gln	Gly	Thr	Leu 140	Val	Thr	Val	Ser	Ser 145	Ala	Ser	Thr	Lys	Gly 150
0	Pro	Ser	Val	Phe	Pro 155	Leu	Ala	Pro	Ser	Ser 160	Lys	Ser	Thr	Ser	Gly 165
Ū	Gly	Thr	Ala	Ala	Leu 170	Gly	Cys	Leu	Val	Lys 175	Asp	Tyr	Phe	Pro	Glu 180
15	Pro	Val	Thr	Val	Ser 185	Trp	Asn	Ser	Gly	Ala 190	Leu	Thr	Ser	Gly	Val 195
	His	Thr	Phe	Pro	Ala 200	Val	Leu	Gln	Ser	Ser 205	Gly	Leu	Tyr	Ser	Leu 210
20	Ser	Ser	Val	Val	Thr 215	Val	Pro	Ser	Ser	Ser 220	Leu	Gly	Thr	Gln	Thr 225
25	Tyr	Ile	Cys	Asn	Val 230	Asn	His	Lys	Pro	Ser 235	Asn	Thr	Lys	Val	Asp 240
25	Lys	Lys	Val	Glu	Pro 245	Lys	Ser	Суѕ	Asp	Lys 250	Thr	His	Thr	Cys	Pro 255
30	Pro 256														
	(2)	INFO	RMAT:	ION I	FOR :	SEQ :	ID N	0:71	:						
35	<b>(</b> :	()	A) LI B) T	ENGTI YPE :	H: 4! Ami:	ACTEI 52 ai no Ac Line	mino cid		ds						
	(x:	i) S	EQUEI	NCE I	DESCI	RIPT	ION:	SEQ	ID I	NO:7	1:				
40	Glu 1	Val	Gln	Leu	Val 5	Gln	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15
45	Gly	Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Tyr	Ser	Phe	Ser 30
	Ser	His	Tyr	Met	His 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly	Leu 45
50	Glu	Trp	Val	Gly	Туг 50	Ile	Asp	Pro	Ser	Asn 55	Gly	Glu	Thr	Thr	Tyr 60
55	Asn	Gln	Lys	Phe	Lys 65	Gly	Arg	Phe	Thr	Leu 70	Ser	Arg	Asp	Asn	Ser 75
55	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser 290		Arg	Ala	Glu	Asp





					80					85					90
	Thr	Ala	Val	Tyr	Tyr 95	Cys	Ala	Arg	Gly	Asp 100	Tyr	Arg	Tyr	Asn	Gly 105
	Asp	Trp	Phe	Phe	Asp 110	Val	Trp	Gly	Gln	Gly 115	Thr	Leu	Val	Thr	Val 120
	Ser	Ser	Ala	Ser	Thr 125	Lys	Gly	Pro	Ser	Val 130	Phe	Pro	Leu	Ala	Pro 135
	Ser	Ser	Lys	Ser	Thr 140	Ser	Gly	Gly	Thr	Ala 145	Ala	Leu	Gly	Cys	Leu 150
	Val	Lys	Asp	Tyr	Phe 155	Pro	Glu	Pro	Val	Thr 160	Val	Ser	Trp	Asn	Ser 165
)	Gly	Ala	Leu	Thr	Ser 170	Gly	Val	His	Thr	Phe 175	Pro	Ala	Val	Leu	Gln 180
J	Ser	Ser	Gly	Leu	Tyr 185	Ser	Leu	Ser	Ser	Val 190	Val	Thr	Val	Pro	Ser 195
.5	Ser	Ser	Leu	Gly	Thr 200	Gln	Thr	Tyr	Ile	Суs 205	Asn	Val	Asn	His	Lys 210
	Pro	Ser	Asn	Thr	Lys 215	Val	Asp	Lys	Lys	Val 220	Glu	Pro	Lys	Ser	Cys 225
30	Asp	Lys	Thr	His	Thr 230	Cys	Pro	Pro	Cys	Pro 235	Ala	Pro	Glu	Leu	Leu 240
35	Gly	Gly	Pro	Ser	Val 245	Phe	Leu	Phe	Pro	Pro 250	Lys	Pro	Lys	Asp	Thr 255
1	Leu	Met	Ile	Ser	Arg 260	Thr	Pro	Glu	Val	Thr 265	Cys	Val	Val	Val	Asp 270
40	Val	Ser	His	Glu	Asp 275	Pro	Glu	Val	Lys	Phe 280	Asn	Trp	Tyr	Val	Asp 285
	Gly	Val	Glu	Val	His 290	Asn	Ala	Lys	Thr	Lys 295	Pro	Arg	Glu	Glu	Gln 300
45	Tyr	Asn	Ser	Thr	Tyr 305	Arg	Val	Val	Ser	Val 310	Leu	Thr	Val	Leu	His 315
50	Gln	Ąsp	Trp	Leu	Asn 320	Gly	Lys	Glu	Tyr	Lys 325	Cys	Lys	Val	Ser	Asn 330
50	Lys	Ala	Leu	Pro	Ala 335	Pro	Ile	Glu	Lys	Thr 340	Ile	Ser	Lys	Ala	Lys 345
55	Gly	Gln	Pro	Arg	Glu 350	Pro	Gln	Val	Tyr	Thr 355	Leu	Pro	Pro	Ser	Arg 360



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Glu Glu Met		ys As 165	n Gln	Val	Ser	Leu 370	Thr	Суѕ	Leu	Val	Lys 375
Gly Phe Tyr	_	Ser As 880	p Ile	Ala	Val	Glu 385	Trp	Glu	Ser	Asn	Gly 390
Gln Pro Glu		Asn Ty 195	r Lys	Thr	Thr	Pro 400	Pro	Val	Leu	Asp	Ser 405
Asp Gly Ser		Phe L∈ 110	eu Tyr	Ser	Lys	Leu 415	Thr	Val	Asp	Lys	Ser 420
Arg Trp Gln		Gly As 125	n Val	Phe	Ser	Суs 430	Ser	Val	Met	His	Glu 435
Ala Leu His		His Ty 140	r Thr	Gln	Lys	Ser 445	Leu	Ser	Leu	Ser	Pro 450
Gly Lys 452											
(2) INFORMAT	ION FO	R SEÇ	ID N	0:72	:						
(A) L (B) T	NCE CH ENGTH: YPE: A OPOLOG	219 Amino	amino Acid		îs						
(xi) SEQUE	NCE DE	ESCRIE	PTIÓN:	SEQ	ID	NO:72	2:				
(xi) SEQUE Asp Ile Gln 1								Ser	Ala	Ser	Val 15
Asp Ile Gln	Met 1	Thr Gl 5	n Ser	Pro	Ser	Ser 10	Leu				15
Asp Ile Gln	Met T	Thr Gl 5 Thr Il 20	n Ser	Pro	Ser	Ser 10 Ser 25	Leu Ser	Gln	Ser	Leu	15 Val 30
Asp Ile Gln 1 Gly Asp Arg	Met T	Thr Gl 5 Thr II 20 Ala Th 35	n Ser e Thr	Pro Cys Leu	Ser Arg His	Ser 10 Ser 25 Trp 40	Leu Ser Tyr	Gln	Ser Gln	Leu Lys	15 Val 30 Pro 45
Asp Ile Gln 1 Gly Asp Arg His Gly Ile	Met T	Thr Gl 5 Thr II 20 Ala Th 35 Lys Le 50	n Ser e Thr ar Tyr	Pro Cys Leu	Ser Arg His	Ser 10 Ser 25 Trp 40 Lys 55	Leu Ser Tyr Val	Gln Gln Ser	Ser Gln Asn	Leu Lys Arg	15 Val 30 Pro 45 Phe 60
Asp Ile Gln 1 Gly Asp Arg His Gly Ile Gly Lys Ala	Met T	Thr Gl 5 Thr III 20 Ala Th 35 Lys Le 50 Ger Ar 65	n Ser e Thr ar Tyr eu Leu	Pro Cys Leu Ile Ser	Ser Arg His Tyr	Ser 10 Ser 25 Trp 40 Lys 55 Ser 70	Leu Ser Tyr Val	Gln Gln Ser	Ser Gln Asn Gly	Leu Lys Arg	15 Val 30 Pro 45 Phe 60 Asp 75
Asp Ile Gln 1 Gly Asp Arg His Gly Ile Gly Lys Ala Ser Gly Val	Met I Val I Gly A Pro L Pro S Thr I	Thr Gl 5 Thr Il 20 Ala Th 35 Les 50 Ger Ar 65	en Ser e Thr Tyr eu Leu eg Phe	Pro Cys Leu Ile Ser Leu	Ser Arg His Tyr Gly	Ser 10 Ser 25 Trp 40 Lys 55 Ser 70 Pro 85	Leu Ser Tyr Val Gly	Gln Gln Ser Ser	Ser Gln Asn Gly Phe	Leu Lys Arg Thr	15 Val 30 Pro 45 Phe 60 Asp 75 Thr 90
Asp Ile Gln 1 Gly Asp Arg His Gly Ile Gly Lys Ala Ser Gly Val Phe Thr Leu	Met To To I see Government of the I see Government of	Thr Gl 5 Thr Il 20 Ala Th 35 Le 50 Ger Ar 65 Ile Se 80 Gln Se	en Ser e Thr Tyr eu Leu er Ser er Thr	Pro Cys Leu Ile Ser Leu His	Ser Arg His Tyr Gly Gln Val	Ser 10 Ser 25 Trp 40 Lys 55 Ser 70 Pro 85 Pro 100	Leu Ser Tyr Val Gly Glu Leu	Gln Gln Ser Ser Asp	Ser Gln Asn Gly Phe	Leu Lys Arg Thr Ala Gly	15 Val 30 Pro 45 Phe 60 Asp 75 Thr 90 Gln 105





Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys 150 145
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  165  Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Leu  Ser Leu
Val Gln Trp Lys  155  155  Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  175  170  175
Glu Ser Val Thr Glu 170  170  Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys 195 190  185
Ser Ser Thr Leu Thi Bed 5 190 185  Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val 210 205
Thr Lys Ser Phe Asn Arg Gly Glu Cys 219 215